Anhangsverzeichnis

Anhang

Tabelle S1: Differenziell exprimierte Proteine von transient transfizierten Caki-2 Zellen bei 100 µM und 20 µM Methionin (mock vs. NNMT)

Spot	Identifikationscode UNIPROT	Bezeichnung	Protein-identifikation	pI	MW in kDa	mock 100 *vs.* NNMT 100	mock 100 *vs.* NNMT 20	mock 100 *vs.* mock 20	mock 20 *vs.* NNMT 20	NNMT 100 *vs.* NNMT 20	mock 20 *vs.* NNMT100
2	P68431	Histone H3.1	H31	11,13	15,3						-2,02
	Q16695	Histone H3.1t	H31T	11,13	15,4						
	Q71DI3	Histone H3.2	H32	11,27	15,4						
	P84243	Histone H3.3	H33	11,27	15,2						
3	Q96A08	Histone H2B type 1-A	H2B1A	10,32	14,0			-2,12			-2,05
	P33778	Histone H2B type 1-B	H2B1B	10,32	13,8						
	P62807	Histone H2B type 1-C/E/F/G/I	H2B1C	10,32	13,8						
	Q99880	Histone H2B type 1-L	H2B1L	10,32	13,8						
	Q8N257	Histone H2B type 3-B	H2B3B	10,32	13,8						
	P57053	Histone H2B type F-S	H2BFS	10,37	13,8						
	P68431	Histone H3.1	H31	11,13	15,3						
	Q16695	Histone H3.1t	H31T	11,13	15,4						
	Q71DI3	Histone H3.2	H32	11,27	15,4						
	P84243	Histone H3.3	H33	11,27	15,2						
6	Q14697	Neutral alpha-glucosidase AB	*GANAB*	5,58	104,0						-5,46
7	**P40261**	**Nicotinamide N-methyltransferase**	**NNMT**	**5,56**	**29,6**	**5,03**	**4,08**		**3,31**		**-4,09**
8	P52565	Rho GDP-dissociation inhibitor 1	GDIR1	5,01	23,1						-2,07
9	O00299	Chloride intracellular channel protein 1	CLIC1	5,09	26,8	2,14					
10	P16949	Stathmin	STMN1	5,76	17,2	2,74					-3,01
	P00441	Superoxide dismutase [Cu-Zn]	SODC	5,7	15,8						
11	P62736	Actin, aortic smooth muscle	ACTA	5,24	41,9	3,18					-5,37
	Q562R1	Beta-actin-like protein 2	ACTBL	5,39	42,0						

Spot	Identifikationscode UNIPROT	Bezeichnung	Protein-identifikation	pI	MW in kDa	mock 100 *vs.* NNMT 100	mock 100 *vs.* NNMT 20	mock 100 *vs.* mock 20	mock 20 *vs.* NNMT 20	NNMT 100 *vs.* NNMT 20	mock 20 *vs.* NNMT100
11	Q6S8J3	POTE ankyrin domain family member E	POTEE	5,83	121,4	3,18					-5,37
	A5A3E0	POTE ankyrin domain family member F	POTEF	5,82	121,4						
	P0CG38	POTE ankyrin domain family member I	POTEI	5,83	121,3						
	Q9BYX7	Putative beta-actin-like protein 3	ACTBM	5,91	42,0						
12	P68133	Actin, alpha skeletal muscle	ACTS	5,23	41,9	3,36					
	P60709	Actin, cytoplasmic 1	ACTB	5,29	41,7						
	P63261	Actin, cytoplasmic 2	ACTG	5,31	41,8						
	P63261	Actin, cytoplasmic 2	ACTG	5,31	41,8						
	Q562R1	Beta-actin-like protein 2	ACTBL	5,39	42,0						
	Q562R1	Beta-actin-like protein 2	ACTBL	5,39	42,0						
	Q6S8J3	POTE ankyrin domain family member E	POTEE	5,83	121,4						
	Q6S8J3	POTE ankyrin domain family member E	POTEE	5,83	121,4						
	A5A3E0	POTE ankyrin domain family member F	POTEF	5,82	121,4						
	A5A3E0	POTE ankyrin domain family member F	POTEF	5,82	121,4						
	P0CG38	POTE ankyrin domain family member I	POTEI	5,83	121,3						
	Q9BYX7	Putative beta-actin-like protein 3	ACTBM	5,91	42,0						
	Q9BYX7	Putative beta-actin-like protein 3	ACTBM	5,91	42,0						
14	P68032	Actin, alpha cardiac muscle 1	ACTC	5,23	41,9	4,12					
	P68133	Actin, alpha skeletal muscle	ACTS	5,23	41,9						
	P62736	Actin, aortic smooth muscle	ACTA	5,24	41,9						
	P60709	Actin, cytoplasmic 1	ACTB	5,29	41,7						
	P63261	Actin, cytoplasmic 2	ACTG	5,31	41,8						
	P63267	Actin, gamma-enteric smooth muscle	ACTH	5,31	41,7						
	Q562R1	Beta-actin-like protein 2	ACTBL	5,39	42,0						

Spot	Identifikationscode UNIPROT	Bezeichnung	Protein-identifikation	pI	MW in kDa	mock 100 *vs.* NNMT 100	mock 100 *vs.* NNMT 20	mock 100 *vs.* mock 20	mock 20 *vs.* NNMT 20	NNMT 100 *vs.* NNMT 20	mock 20 *vs.* NNMT 100
14	Q6S8J3	POTE ankyrin domain family member E	POTEE	5,83	121,4	4,12					
	A5A3E0	POTE ankyrin domain family member F	POTEF	5,82	121,4						
	P0CG38	POTE ankyrin domain family member I	POTEI	5,83	121,3						
	Q9BYX7	Putative beta-actin-like protein 3	ACTBM	5,91	42,0						
15	P61158	Actin-related protein 3	ARP3	5,61	47,2		2,22				
16	P30101	Protein disulfide-isomerase A3	PDIA3	5,61	54,3	2,08	2,20				
17	P16949	Stathmin	STMN1	5,76	17,2		2,21		2,12	-2,03	
18	P08670	Vimentin	VIME	5,05	53,5		3,62		2,19		
19	P62736	Actin, aortic smooth muscle	ACTA	5,24	41,9	-4,96					
	P60709	Actin, cytoplasmic 1	ACTB	5,29	41,7						
	P63261	Actin, cytoplasmic 2	ACTG	5,31	41,8						
	Q562R1	Beta-actin-like protein 2	ACTBL	5,39	42,0						
	Q6S8J3	POTE ankyrin domain family member E	POTEE	5,83	121,4						
	A5A3E0	POTE ankyrin domain family member F	POTEF	5,82	121,4						
	P0CG38	POTE ankyrin domain family member I	POTEI	5,83	121,3						
	Q9BYX7	Putative beta-actin-like protein 3	ACTBM	5,91	42,0						
20	P08758	Annexin A5	ANXA5	4,93	35,8	-4,90	-3,10	-4,98			
21	O75083	WD repeat-containing protein 1	WDR1	6,17	66,2	-2,18					2,39
	P12956	X-ray repair cross-complementing protein 6	XRCC6	6,23	69,7						
22	P05388	60S acidic ribosomal protein P0	RLA0	5,7	34,3	-2,08					
	Q8NHW5	60S acidic ribosomal protein P0-like	RLA0L	5,39	34,4						
	Q9HB07	UPF0160 protein MYG1, mitochondrial	MYG1	5,5	37,1						
23	P11413	Glucose-6-phosphate 1-dehydrogenase	G6PD	6,41	59,1	-2,01					

Spot	Identifikationscode UNIPROT	Bezeichnung	Protein-identifikation	pI	MW in kDa	mock 100 *vs.* NNMT 100	mock 100 *vs.* NNMT 20	mock 100 *vs.* mock 20	mock 20 *vs.* NNMT 20	NNMT 100 *vs.* NNMT 20	mock 20 *vs.* NNMT 100
24	Q96KP4	Cytosolic non-specific dipeptidase	CNDP2	5,66	52,7	-2,03					
	P23381	Tryptophan--tRNA ligase, cytoplasmic	SYWC	5,83	53,0						
25	P42704	Leucine-rich PPR motif-containing protein, mitochondrial	LPPRC	5,53	151,8			-2,15			
27	Q14697	Neutral alpha-glucosidase AB	GANAB	5,58	104,0			-7,80			-9,28
28	P15311	Ezrin	EZRI	5,94	69,4			-2,66			
	P26038	Moesin	MOES	6,09	67,7						
	P35241	Radixin	RADI	6,03	68,6						
29	P07237	Protein disulfide-isomerase	PDIA1	4,69	55,3			-2,10			
30	P62736	Actin, aortic smooth muscle	ACTA	5,24	41,9			-2,04			
	P63261	Actin, cytoplasmic 2	ACTG	5,31	41,8						
	Q562R1	Beta-actin-like protein 2	ACTBL	5,39	42,0						
	O60664	Perilipin-3	PLIN3	5,3	46,9						
	Q6S8J3	POTE ankyrin domain family member E	POTEE	5,83	121,4						
	A5A3E0	POTE ankyrin domain family member F	POTEF	5,82	121,4						
	Q9BYX7	Putative beta-actin-like protein 3	ACTBM	5,91	42,0						
31	P08865	40S ribosomal protein SA	RSSA	4,79	32,7			-2,10			
	P08865	40S ribosomal protein SA	RSSA	4,79	32,7						
32	Q04828	Aldo-keto reductase family 1 member C1	AK1C1	8,02	36,8	-2,15	-5,74	-2,11	-2,72	2,68	
	P52895	Aldo-keto reductase family 1 member C2	AK1C2	7,13	36,7						
	P42330	Aldo-keto reductase family 1 member C3	AK1C3	8,06	36,9						
34	P07900	Heat shock protein HSP 90-alpha	HS90A	4,94	84,5		-2,01				
	P08238	Heat shock protein HSP 90-beta	HS90B	4,96	83,1						
	Q58FF6	Putative heat shock protein HSP 90-beta 4	H90B4	4,65	58,3						
	Q58FF7	Putative heat shock protein HSP 90-beta-3	H90B3	4,71	68,3						

Spot	Identifikationscode UNIPROT	Bezeichnung	Protein-identifikation	pI	MW in kDa	mock 100 *vs.* NNMT 100	mock 100 *vs.* NNMT 20	mock 100 *vs.* mock 20	mock 20 *vs.* NNMT 20	NNMT 100 *vs.* NNMT 20	mock 20 *vs.* NNMT 100
36	P0DMV9	Heat shock 70 kDa protein 1B	HS71B	5,48	69,9		-4,76				
	P34931	Heat shock 70 kDa protein 1-like	HS71L	5,75	70,4						
	P11142	Heat shock cognate 71 kDa protein	HSP7C	5,37	70,8						
	P54652	Heat shock-related 70 kDa protein 2	HSP72	5,55	70,0						
38	P61978	Heterogeneous nuclear ribonucleoprotein K	HNRPK	5,39	51,0		-2,81	-2,25			
39	P31939	Bifunctional purine biosynthesis protein PURH	PUR9	6,27	64,6		-2,65		-3,65	3,68	
40	O75390	Citrate synthase, mitochondrial	CISY	7,39	49,0		-2,15				
	P00558	Phosphoglycerate kinase 1	PGK1	8,3	44,5						
41	P09972	Fructose-bisphosphate aldolase C	ALDOC	6,41	39,5	-2,18	-2,20				
	P09651	Heterogeneous nuclear ribonucleoprotein A1	ROA1	9,17	38,7						
	Q14103	Heterogeneous nuclear ribonucleoprotein D0	HNRPD	7,6	38,3						
	O14979	Heterogeneous nuclear ribonucleoprotein D-like	HNRDL	9,59	46,4						
	Q15365	Poly(rC)-binding protein 1	PCBP1	6,66	37,5						
42	P68104	Elongation factor 1-alpha 1	EF1A1	9,1	50,0						2,01
	P26599	Polypyrimidine tract-binding protein 1	PTBP1	9,22	57,2						
	Q5VTE0	Putative elongation factor 1-alpha-like 3	EF1A3	9,15	50,1						
44	P08758	Annexin A5	ANXA5	4,93	35,8	-3,01					5,06
	Q15691	Microtubule-associated protein RP/EB family member 1	MARE1	5,02	29,9						
45	P09651	Heterogeneous nuclear ribonucleoprotein A1	ROA1	9,17	38,7	-3,19					2,17
46	P09429	High mobility group protein B1	HMGB1	5,6	24,9						3,02
	P26583	High mobility group protein B2	HMGB2	7,62	24,0						
	B2RPK0	Putative high mobility group protein B1-like 1	HGB1A	5,91	24,2						
48	Q14697	Neutral alpha-glucosidase AB	GANAB	5,58	104,0			2,32			

Spot	Identifikationscode UNIPROT	Bezeichnung	Protein-identifikation	pI	MW in kDa	mock 100 *vs.* NNMT 100	mock 100 *vs.* NNMT 20	mock 100 *vs.* mock 20	mock 20 *vs.* NNMT 20	NNMT 100 *vs.* NNMT 20	mock 20 *vs.* NNMT 100
49	A5D8W1	Cilia- and flagella-associated protein 69	CFA69	6,81	105,9			2,66			
	P13010	X-ray repair cross-complementing protein 5	XRCC5	5,55	82,6						
50	P68032	Actin, alpha cardiac muscle 1	ACTC	5,23	41,9			2,17			
	P68133	Actin, alpha skeletal muscle	ACTS	5,23	41,9						
51	P63261	Actin, cytoplasmic 2	ACTG	5,31	41,8		5,28	6,48			
	Q562R1	Beta-actin-like protein 2	ACTBL	5,39	42,0						
	Q6S8J3	POTE ankyrin domain family member E	POTEE	5,83	121,4						
	A5A3E0	POTE ankyrin domain family member F	POTEF	5,82	121,4						
	Q9BYX7	Putative beta-actin-like protein 3	ACTBM	5,91	42,0						
52	P52597	Heterogeneous nuclear ribonucleoprotein F	HNRPF	5,37	45,7			2,08			
	P31943	Heterogeneous nuclear ribonucleoprotein H	HNRH1	5,89	49,2						
	P55795	Heterogeneous nuclear ribonucleoprotein H2	HNRH2	5,89	49,3						
53	P68032	Actin, alpha cardiac muscle 1	ACTC	5,23	41,9			2,34			3,03
	P60709	Actin, cytoplasmic 1	ACTB	5,29	41,7						
	P63261	Actin, cytoplasmic 2	ACTG	5,31	41,8						
	Q562R1	Beta-actin-like protein 2	ACTBL	5,39	42,0						
	Q6S8J3	POTE ankyrin domain family member E	POTEE	5,83	121,4						
	A5A3E0	POTE ankyrin domain family member F	POTEF	5,82	121,4						
	P0CG38	POTE ankyrin domain family member I	POTEI	5,83	121,3						
	Q9BYX7	Putative beta-actin-like protein 3	ACTBM	5,91	42,0						
	Q13148	TAR DNA-binding protein 43	TADBP	5,85	44,7						

Tabelle S2: Differenziell exprimierte Proteine von transient transfizierten HEK-293 Zellen bei 100 µM Methionin (mock *vs*. NNMT)

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
1	Q9C0C9	(E3-independent) E2 ubiquitin-conjugating enzyme	UBE2O	141,2	5,12	1,89
2	O75832	26S proteasome non-ATPase regulatory subunit 10	PSMD10	24,4	6,10	0,57
3	Q9UNM6	26S proteasome non-ATPase regulatory subunit 13	PSMD13	42,9	5,81	1,93
4	P51398	28S ribosomal protein S29, mitochondrial	DAP3	45,5	8,88	2,02
5	P82933	28S ribosomal protein S9, mitochondrial	MRPS9	45,8	9,51	0,50
6	P12694	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	BCKDHA	50,4	8,27	0,65
7	Q9H9J2	39S ribosomal protein L44, mitochondrial	MRPL44	37,5	8,40	3,55
8	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	26,9	7,78	0,29
9	P62841	40S ribosomal protein S15	RPS15	17,0	10,39	1,51
10	P62249	40S ribosomal protein S16	RPS16	16,4	10,21	1,80
11	P15880	40S ribosomal protein S2	RPS2	31,3	10,24	2,09
12	P62266	40S ribosomal protein S23	RPS23	15,8	10,49	1,61
13	P23396	40S ribosomal protein S3	RPS3	26,7	9,66	1,77
14	P10155	60 kDa SS-A/Ro ribonucleoprotein	TROVE2	60,6	8,03	1,96
15	P18621	60S ribosomal protein L17	RPL17	21,4	10,17	1,50
16	Q9Y3U8	60S ribosomal protein L36	RPL36	12,2	11,59	0,66
17	O15143	Actin-related protein 2/3 complex subunit 1B	ARPC1B	40,9	8,35	hoch
18	O15145	Actin-related protein 2/3 complex subunit 3	ARPC3	20,5	8,59	1,70
19	P07108	Acyl-CoA-binding protein	DBI	10,0	6,57	0,32
20	P46108	Adapter molecule crk	CRK	33,8	5,55	0,64
21	P55263	Adenosine kinase	ADK	40,5	6,70	runter
22	P23526	Adenosylhomocysteinase	AHCY	47,7	6,34	1,70
23	O43865	Adenosylhomocysteinase 2	AHCYL1	58,9	6,89	runter
24	P05141	ADP/ATP translocase 2	SLC25A5	32,8	9,69	0,21
25	P12236	ADP/ATP translocase 3	SLC25A6	32,8	9,74	0,13
26	P84077	ADP-ribosylation factor 1	ARF1	20,7	6,80	1,70
27	P61204	ADP-ribosylation factor 3	ARF3	20,6	7,43	1,70
28	P62330	ADP-ribosylation factor 6	ARF6	20,1	8,95	hoch
29	Q9Y4W6	AFG3-like protein 2	AFG3L2	88,5	8,66	0,60
30	P14550	Alcohol dehydrogenase [NADP(+)]	AKR1A1	36,6	6,79	1,62
31	Q8IZ83	Aldehyde dehydrogenase family 16 member A1	ALDH16A1	85,1	6,79	2,27
32	Q96C23	Aldose 1-epimerase	GALM	37,7	6,65	1,67
33	P15121	Aldose reductase	AKR1B1	35,8	6,98	1,58
34	P37840	Alpha-synuclein	SNCA	14,5	4,70	runter
35	P40222	Alpha-taxilin	TXLNA	61,9	6,52	0,63

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
36	Q6FI81	Anamorsin	CIAPIN1	33,6	5,62	2,18
37	P50995	Annexin A11	ANXA11	54,4	7,65	1,50
38	P08133	Annexin A6	ANXA6	75,8	5,60	1,85
39	O94973	AP-2 complex subunit alpha-2	AP2A2	103,9	6,96	0,62
40	O95831	Apoptosis-inducing factor 1, mitochondrial	AIFM1	66,9	8,95	1,72
41	Q6PI48	Aspartate--tRNA ligase, mitochondrial	DARS2	73,5	8,02	1,60
42	Q15121	Astrocytic phosphoprotein PEA-15	A15	15,0	5,02	1,66
43	Q9UBB4	Ataxin-10	ATXN10	53,5	5,25	0,64
44	P24539	ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	28,9	9,36	hoch
45	P36542	ATP synthase subunit gamma, mitochondrial	ATP5C1	33,0	9,22	2,19
46	O75027	ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	82,6	9,33	0,41
47	P28288	ATP-binding cassette sub-family D member 3	ABCD3	75,4	9,36	0,55
48	P53396	ATP-citrate synthase	ACLY	120,8	7,33	0,56
49	Q9UMR2	ATP-dependent RNA helicase DDX19B	DDX19B	53,9	6,30	0,66
50	O95816	BAG family molecular chaperone regulator 2	BAG2	23,8	6,70	hoch
51	O43491	Band 4.1-like protein 2	EPB41L2	112,5	5,44	0,53
52	Q9Y6E2	Basic leucine zipper and W2 domain-containing protein 2	BZW2	48,1	6,68	3,46
53	Q9NYF8	Bcl-2-associated transcription factor 1	BCLAF1	106,1	9,98	0,44
54	P61769	Beta-2-microglobulin	B2M	13,7	6,52	0,63
55	Q562R1	Beta-actin-like protein 2	ACTBL2	42,0	5,59	36,00
56	P42025	Beta-centractin	ACTR1B	42,3	6,40	hoch
57	P55957	BH3-interacting domain death agonist	BID	22,0	5,44	1,72
58	P17655	Calpain-2 catalytic subunit	CAPN2	79,9	4,98	0,55
59	Q99439	Calponin-2	CNN2	33,7	7,33	1,74
60	P30622	CAP-Gly domain-containing linker protein 1	CLIP1	162,1	5,36	runter
61	Q14444	Caprin-1	CAPRIN1	78,3	5,25	0,60
62	O75976	Carboxypeptidase D	CPD	152,8	6,05	runter
63	P19784	Casein kinase II subunit alpha'	CSNK2A2	41,2	8,56	0,59
64	P42574	Caspase-3	CASP3	31,6	6,54	0,54
65	P35222	Catenin beta-1	CTNNB1	85,4	5,86	runter
66	P07858	Cathepsin B	CTSB	37,8	6,30	2,50
67	Q9NX58	Cell growth-regulating nucleolar protein	LYAR	43,6	9,54	1,88
68	Q14839	Chromodomain-helicase-DNA-binding protein 4	CHD4	217,9	5,86	0,57
69	O43809	Cleavage and polyadenylation specificity factor subunit 5	NUDT21	26,2	8,82	1,61
70	P35606	Coatomer subunit beta'	COPB2	102,4	5,27	0,58
71	Q4VC31	Coiled-coil domain-containing protein 58	CCDC58	16,6	7,81	1,68
72	Q15021	Condensin complex subunit 1	NCAPD2	157,1	6,61	1,85

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
73	Q9BR76	Coronin-1B	CORO1B	54,2	5,88	0,63
74	Q13363	C-terminal-binding protein 1	CTBP1	47,5	6,77	1,50
75	P08574	Cytochrome c1, heme protein, mitochondrial	CYC1	35,4	9,00	0,35
76	Q14204	Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	532,1	6,40	0,54
77	Q96KP4	Cytosolic non-specific dipeptidase	CNDP2	52,8	5,97	0,47
78	O43175	D-3-phosphoglycerate dehydrogenase	PHGDH	56,6	6,71	1,59
79	Q5BKZ1	DBIRD complex subunit ZNF326	ZNF326	65,6	5,15	0,59
80	Q9Y3Z3	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	72,2	7,14	3,26
81	P15924	Desmoplakin	DSP	331,6	6,81	0,46
82	P60981	Destrin	DSTN	18,5	7,85	1,76
83	Q14195	Dihydropyrimidinase-related protein 3	DPYSL3	61,9	6,49	0,63
84	Q9NY33	Dipeptidyl peptidase 3	DPP3	82,5	5,10	0,62
85	P43246	DNA mismatch repair protein Msh2	MSH2	104,7	5,77	1,74
86	P52701	DNA mismatch repair protein Msh6	MSH6	152,7	6,90	0,65
87	Q96EY1	DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	52,5	9,26	0,61
88	Q9NVH1	DnaJ homolog subfamily C member 11	DNAJC11	63,2	8,40	1,65
89	O60762	Dolichol-phosphate mannosyltransferase subunit 1	DPM1	29,6	9,57	0,60
90	P04844	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	69,2	5,69	2,02
91	Q02750	Dual specificity mitogen-activated protein kinase kinase 1	MAP2K1	43,4	6,62	0,57
92	P36507	Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	44,4	6,55	runter
93	Q14203	Dynactin subunit 1	DCTN1	141,6	5,81	0,64
94	O60313	Dynamin-like 120 kDa protein, mitochondrial	OPA1	111,6	7,87	1,52
95	P63167	Dynein light chain 1, cytoplasmic	DYNLL1	10,4	7,40	0,29
96	Q99496	E3 ubiquitin-protein ligase RING2	RNF2	37,6	6,84	1,70
97	O94874	E3 UFM1-protein ligase 1	UFL1	89,5	6,79	0,60
98	Q96C19	EF-hand domain-containing protein D2	EFHD2	26,7	5,20	0,40
99	Q9H4M9	EH domain-containing protein 1	EHD1	60,6	6,83	0,62
100	Q9NZN3	EH domain-containing protein 3	EHD3	60,8	6,57	0,65
101	Q8IUD2	ELKS/Rab6-interacting/CAST family member 1	ERC1	128,0	5,97	1,53
102	P43897	Elongation factor Ts, mitochondrial	TSFM	35,4	8,38	1,54
103	P50402	Emerin	EMD	29,0	5,50	1,80
104	Q53H82	Endoribonuclease LACTB2	LACTB2	32,8	6,80	1,68
105	Q96F86	Enhancer of mRNA-decapping protein 3	EDC3	56,0	7,11	1,71
106	P42126	Enoyl-CoA delta isomerase 1, mitochondrial	ECI1	32,8	8,54	1,95
107	P29317	Ephrin type-A receptor 2	EPHA2	108,2	6,23	2,47
108	Q9UBC2	Epidermal growth factor receptor substrate 15-like 1	EPS15L1	94,2	5,11	0,61

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
109	P15170	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	GSPT1	55,7	5,62	1,57
110	Q8IYD1	Eukaryotic peptide chain release factor GTP-binding subunit ERF3B	GSPT2	68,8	5,43	2,06
111	P62495	Eukaryotic peptide chain release factor subunit 1	ETF1	49,0	5,71	0,59
112	P55884	Eukaryotic translation initiation factor 3 subunit B	EIF3B	92,4	5,00	1,67
113	Q9UBQ5	Eukaryotic translation initiation factor 3 subunit K	EIF3K	25,0	4,93	1,95
114	P23588	Eukaryotic translation initiation factor 4B	EIF4B	69,1	5,73	0,45
115	P06730	Eukaryotic translation initiation factor 4E	EIF4E	25,1	6,15	0,66
116	Q13868	Exosome complex component RRP4	EXOSC2	32,8	7,50	1,72
117	Q9UIA9	Exportin-7	XPO7	123,8	6,32	0,59
118	Q9BSJ8	Extended synaptotagmin-1	ESYT1	122,8	5,83	0,57
119	P47755	F-actin-capping protein subunit alpha-2	CAPZA2	32,9	5,85	0,55
120	P02794	Ferritin heavy chain	FTH1	21,2	5,55	runter
121	O75955	Flotillin-1	FLOT1	47,3	7,49	1,77
122	P51116	Fragile X mental retardation syndrome-related protein 2	FXR2	74,2	6,23	0,32
123	Q9BQ67	Glutamate-rich WD repeat-containing protein 1	GRWD1	49,4	4,92	2,24
124	P28161	Glutathione S-transferase Mu 2	GSTM2	25,7	6,37	1,66
125	P09211	Glutathione S-transferase P	GSTP1	23,3	5,64	1,92
126	Q8NBJ4	Golgi membrane protein 1	GOLM1	45,3	4,97	runter
127	Q9H4A6	Golgi phosphoprotein 3	GOLPH3	33,8	6,44	0,61
128	Q12849	G-rich sequence factor 1	GRSF1	53,1	6,19	runter
129	Q14C86	GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1	164,9	5,22	1,95
130	P29992	Guanine nucleotide-binding protein subunit alpha-11	GNA11	42,1	5,69	1,50
131	Q9Y450	HBS1-like protein	HBS1L	75,4	6,61	runter
132	P51858	Hepatoma-derived growth factor	HDGF	26,8	4,73	0,63
133	Q7Z4V5	Hepatoma-derived growth factor-related protein 2	HDGFRP2	74,3	7,49	2,30
134	Q9Y3E1	Hepatoma-derived growth factor-related protein 3	HDGFRP3	22,6	7,99	0,49
135	Q5SSJ5	Heterochromatin protein 1-binding protein 3	HP1BP3	61,2	9,67	0,66
136	O14979	Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	46,4	9,57	0,60
137	P31943	Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	49,2	6,30	0,64
138	Q8WVV9	Heterogeneous nuclear ribonucleoprotein L-like	HNRNPLL	60,0	7,72	1,99
139	P26583	High mobility group protein B2	HMGB2	24,0	7,81	0,59
140	P17096	High mobility group protein HMG-I/HMG-Y	HMGA1	11,7	10,32	0,66
141	P12081	Histidine--tRNA ligase, cytoplasmic	HARS	57,4	5,88	0,66
142	P62805	Histone H4	HIST1H4A	11,4	11,36	1,75
143	Q16576	Histone-binding protein RBBP7	RBBP7	47,8	5,05	1,85

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144	Q16543	Hsp90 co-chaperone Cdc37	CDC37	44,4	5,25	9,25
145	O00629	Importin subunit alpha-3	KPNA4	57,9	4,96	2,30
146	O95373	Importin-7	IPO7	119,4	4,82	1,87
147	P29218	Inositol monophosphatase 1	IMPA1	30,2	5,26	1,59
148	P05556	Integrin beta-1	ITGB1	88,4	5,39	0,64
149	Q13418	Integrin-linked protein kinase	ILK	51,4	8,07	1,85
150	P41252	Isoleucine--tRNA ligase, cytoplasmic	IARS	144,4	6,15	0,62
151	Q13907	Isopentenyl-diphosphate Delta-isomerase 1	IDI1	26,3	6,34	hoch
152	P14923	Junction plakoglobin	JUP	81,7	6,14	0,38
153	Q96EK5	KIF1-binding protein	KIF1BP	71,8	5,49	0,54
154	Q9NSK0	Kinesin light chain 4	KLC4	68,6	6,18	runter
155	Q14739	Lamin-B receptor	LBR	70,7	9,36	0,57
156	Q01650	Large neutral amino acids transporter small subunit 1	SLC7A5	55,0	7,72	1,62
157	P46379	Large proline-rich protein BAG6	BAG6	119,3	5,60	0,56
158	Q86V48	Leucine zipper protein 1	LUZP1	120,2	8,50	runter
159	Q14847	LIM and SH3 domain protein 1	LASP1	29,7	7,05	0,64
160	P00338	L-lactate dehydrogenase A chain	LDHA	36,7	8,27	1,75
161	P10253	Lysosomal alpha-glucosidase	GAA	105,3	6,00	runter
162	Q9NZW5	MAGUK p55 subfamily member 6	MPP6	61,1	6,18	runter
163	Q3KQU3	MAP7 domain-containing protein 1	MAP7D1	92,8	10,11	1,51
164	P55081	Microfibrillar-associated protein 1	MFAP1	51,9	4,98	1,57
165	Q66K74	Microtubule-associated protein 1S	MAP1S	112,1	7,30	0,56
166	Q8TCT9	Minor histocompatibility antigen H13	HM13	41,5	6,43	0,51
167	O96008	Mitochondrial import receptor subunit TOM40 homolog	TOMM40	37,9	7,25	0,63
168	Q8IXI1	Mitochondrial Rho GTPase 2	RHOT2	68,1	5,86	runter
169	Q9Y3A3	MOB-like protein phocein	MOB4	26,0	5,78	4,28
170	P53985	Monocarboxylate transporter 1	SLC16A1	53,9	8,66	1,72
171	Q13423	NAD(P) transhydrogenase, mitochondrial	NNT	113,8	8,09	1,76
172	Q8NCW5	NAD(P)H-hydrate epimerase	NAXE	31,7	7,66	2,12
173	Q9NXA8	NAD-dependent protein deacylase sirtuin-5, mitochondrial	SIRT5	33,9	8,47	1,93
174	O95299	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	40,7	8,48	0,66
175	O75251	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	23,5	9,99	0,38
176	P48163	NADP-dependent malic enzyme	ME1	64,1	6,13	1,74
177	Q13564	NEDD8-activating enzyme E1 regulatory subunit	NAE1	60,2	5,40	0,44
178	Q8WX92	Negative elongation factor B	NELFB	65,7	6,13	hoch
179	Q9BYT8	Neurolysin, mitochondrial	NLN	80,6	6,64	0,60

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
180	Q9Y639	Neuroplastin	NPTN	44,4	7,99	runter
181	Q15758	Neutral amino acid transporter B(0)	SLC1A5	56,6	5,48	0,53
182	Q96TA1	Niban-like protein 1	FAM129B	84,1	6,19	runter
183	**P40261**	**Nicotinamide N-methyltransferase**	**NNMT**	**29,6**	**5,74**	**hoch**
184	Q15155	Nodal modulator 1	NOMO1	134,2	5,81	0,45
185	Q5JPE7	Nodal modulator 2	NOMO2	139,4	5,76	0,45
186	P69849	Nodal modulator 3	NOMO3	134,0	5,67	0,45
187	Q9NXR1	Nuclear distribution protein nudE homolog 1	NDE1	38,8	5,27	0,38
188	P57740	Nuclear pore complex protein Nup107	NUP107	106,3	5,43	0,39
189	Q9UKX7	Nuclear pore complex protein Nup50	NUP50	50,1	7,06	1,67
190	Q14978	Nucleolar and coiled-body phosphoprotein 1	NOLC1	73,6	9,47	2,80
191	Q8NFH5	Nucleoporin NUP53	NUP35	34,8	9,09	0,38
192	P12270	Nucleoprotein TPR	TPR	267,1	5,02	0,66
193	Q99733	Nucleosome assembly protein 1-like 4	NAP1L4	42,8	4,69	1,72
194	Q9NQR4	Omega-amidase NIT2	NIT2	30,6	7,21	1,71
195	P22059	Oxysterol-binding protein 1	OSBP	89,4	7,30	0,57
196	Q15645	Pachytene checkpoint protein 2 homolog	TRIP13	48,5	6,09	0,59
197	P50897	Palmitoyl-protein thioesterase 1	PPT1	34,2	6,52	0,61
198	O75475	PC4 and SFRS1-interacting protein	PSIP1	60,1	9,13	1,63
199	O14908	PDZ domain-containing protein GIPC1	GIPC1	36,0	6,28	runter
200	Q96AY3	Peptidyl-prolyl cis-trans isomerase FKBP10	FKBP10	64,2	5,62	0,51
201	P26885	Peptidyl-prolyl cis-trans isomerase FKBP2	FKBP2	15,6	9,13	2,07
202	Q9H2H8	Peptidyl-prolyl cis-trans isomerase-like 3	PPIL3	18,1	6,79	0,14
203	Q8WW12	PEST proteolytic signal-containing nuclear protein	PCNP	18,9	7,49	0,61
204	Q13492	Phosphatidylinositol-binding clathrin assembly protein	PICALM	70,7	7,90	1,60
205	O95394	Phosphoacetylglucosamine mutase	PGM3	59,8	6,25	0,35
206	Q14558	Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	39,4	7,20	hoch
207	O15067	Phosphoribosylformylglycinamidine synthase	PFAS	144,6	5,76	0,62
208	P78330	Phosphoserine phosphatase	PSPH	25,0	5,69	1,73
209	Q6NYC8	Phostensin	PPP1R18	67,9	5,40	runter
210	O15031	Plexin-B2	PLXNB2	205,0	6,24	runter
211	Q86U42	Polyadenylate-binding protein 2	PABPN1	32,7	5,06	1,50
212	O60828	Polyglutamine-binding protein 1	PQBP1	30,5	6,33	0,57
213	Q6NZI2	Polymerase I and transcript release factor	PTRF	43,5	5,60	1,61
214	O95758	Polypyrimidine tract-binding protein 3	PTBP3	59,7	9,04	1,56
215	Q9UHV9	Prefoldin subunit 2	PFDN2	16,6	6,58	0,55
216	Q6UN15	Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	66,5	5,59	0,65

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217	Q9UHG3	Prenylcysteine oxidase 1	PCYOX1	56,6	6,18	0,48
218	Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	83,5	6,95	0,57
219	O75340	Programmed cell death protein 6	PDCD6	21,9	5,40	1,68
220	Q99623	Prohibitin-2	PHB2	33,3	9,83	2,44
221	P48147	Prolyl endopeptidase	PREP	80,6	5,86	1,63
222	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial	PCCA	80,0	7,52	0,48
223	P07602	Prosaposin	PSAP	58,1	5,17	0,52
224	Q14914	Prostaglandin reductase 1	PTGR1	35,8	8,29	1,72
225	P25788	Proteasome subunit alpha type-3	PSMA3	28,4	5,33	0,60
226	P28066	Proteasome subunit alpha type-5	PSMA5	26,4	4,79	1,74
227	P49721	Proteasome subunit beta type-2	PSMB2	22,8	7,02	2,07
228	Q5VYK3	Proteasome-associated protein ECM29 homolog	ECM29	204,2	7,12	0,31
229	Q99873	Protein arginine N-methyltransferase 1	PRMT1	41,5	5,43	1,54
230	O14744	Protein arginine N-methyltransferase 5	PRMT5	72,6	6,29	0,61
231	Q9UFN0	Protein NipSnap homolog 3A	NIPSNAP3A	28,4	9,16	1,65
232	Q15435	Protein phosphatase 1 regulatory subunit 7	PPP1R7	41,5	4,91	1,90
233	P29590	Protein PML	PML	97,5	6,21	0,36
234	P31949	Protein S100-A11	S100A11	11,7	7,12	0,35
235	Q15436	Protein transport protein Sec23A	SEC23A	86,1	7,08	0,63
236	Q9H3U1	Protein unc-45 homolog A	UNC45A	103,0	6,07	1,57
237	P22061	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	24,6	7,21	1,50
238	P06454	Prothymosin alpha	PTMA	12,2	3,78	0,12
239	Q14671	Pumilio homolog 1	PUM1	126,4	6,84	0,60
240	P00491	Purine nucleoside phosphorylase	PNP	32,1	6,95	1,63
241	Q58FG0	Putative heat shock protein HSP 90-alpha A5	HSP90AA5P	38,7	6,57	1,85
242	B2RPK0	Putative high mobility group protein B1-like 1	HMGB1P1	24,2	6,21	1,74
243	Q9Y383	Putative RNA-binding protein Luc7-like 2	LUC7L2	46,5	10,01	0,55
244	Q6P996	Pyridoxal-dependent decarboxylase domain-containing protein 1	PDXDC1	86,7	5,38	1,76
245	Q15276	Rab GTPase-binding effector protein 1	RABEP1	99,2	5,01	0,59
246	Q9H6Z4	Ran-binding protein 3	RANBP3	60,2	4,78	0,65
247	P61026	Ras-related protein Rab-10	RAB10	22,5	8,38	hoch
248	Q8WUD1	Ras-related protein Rab-2B	RAB2B	24,2	7,83	1,62
249	Q15286	Ras-related protein Rab-35	RAB35	23,0	8,29	0,43
250	P51149	Ras-related protein Rab-7a	RAB7A	23,5	6,70	1,71
251	P61006	Ras-related protein Rab-8A	RAB8A	23,7	9,07	1,57
252	Q92900	Regulator of nonsense transcripts 1	UPF1	124,3	6,61	0,39
253	Q07960	Rho GTPase-activating protein 1	ARHGAP1	50,4	6,29	0,61

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254	O75792	Ribonuclease H2 subunit A	RNASEH2A	33,4	5,25	1,62
255	P13489	Ribonuclease inhibitor	RNH1	49,9	4,82	1,77
256	Q7LG56	Ribonucleoside-diphosphate reductase subunit M2 B	RRM2B	40,7	4,97	runter
257	O76021	Ribosomal L1 domain-containing protein 1	RSL1D1	54,9	10,13	0,62
258	Q15418	Ribosomal protein S6 kinase alpha-1	RPS6KA1	82,7	7,83	runter
259	P51812	Ribosomal protein S6 kinase alpha-3	RPS6KA3	83,7	6,89	0,64
260	Q8TDN6	Ribosome biogenesis protein BRX1 homolog	BRIX1	41,4	9,92	0,32
261	Q15050	Ribosome biogenesis regulatory protein homolog	RRS1	41,2	10,70	1,65
262	Q9H0A0	RNA cytidine acetyltransferase	NAT10	115,7	8,27	1,54
263	Q9H6T3	RNA polymerase II-associated protein 3	RPAP3	75,7	6,84	0,55
264	P98179	RNA-binding protein 3	RBM3	17,2	8,91	0,55
265	Q15424	Scaffold attachment factor B1	SAFB	102,6	5,47	0,64
266	Q12765	Secernin-1	SCRN1	46,4	4,75	1,53
267	Q16629	Serine/arginine-rich splicing factor 7	SRSF7	27,4	11,82	0,56
268	P61011	Signal recognition particle 54 kDa protein	SRP54	55,7	8,75	0,53
269	Q9Y5M8	Signal recognition particle receptor subunit beta	SRPRB	29,7	9,04	hoch
270	P42224	Signal transducer and activator of transcription 1-alpha/beta	STAT1	87,3	6,05	runter
271	Q13573	SNW domain-containing protein 1	SNW1	61,5	9,52	1,72
272	Q13596	Sorting nexin-1	SNX1	59,0	5,15	1,57
273	Q9UMY4	Sorting nexin-12	SNX12	19,7	7,87	2,18
274	O60493	Sorting nexin-3	SNX3	18,8	8,66	runter
275	Q9UNH7	Sorting nexin-6	SNX6	46,6	6,16	0,64
276	Q8N0X7	Spartin	SPG20	72,8	5,91	2,00
277	Q13813	Spectrin alpha chain, non-erythrocytic 1	SPTAN1	284,4	5,35	0,66
278	P19623	Spermidine synthase	SRM	33,8	5,49	1,50
279	Q15393	Splicing factor 3B subunit 3	SF3B3	135,5	5,26	1,59
280	Q9GZT3	SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP	12,3	10,24	runter
281	P35610	Sterol O-acyltransferase 1	SOAT1	64,7	8,94	1,94
282	Q9UJZ1	Stomatin-like protein 2, mitochondrial	STOML2	38,5	7,39	1,56
283	P31948	Stress-induced-phosphoprotein 1	STIP1	62,6	6,80	0,64
284	O95347	Structural maintenance of chromosomes protein 2	SMC2	135,6	8,43	2,03
285	P51649	Succinate-semialdehyde dehydrogenase, mitochondrial	ALDH5A1	57,2	8,28	2,04
286	P0DMN0	Sulfotransferase 1A4	SULT1A4	34,2	6,01	1,62
287	P63279	SUMO-conjugating enzyme UBC9	UBE2I	18,0	8,66	1,69
288	Q12824	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1	SMARCB1	44,1	6,23	0,48
289	Q969G3	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	SMARCE1	46,6	4,88	5,16

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290	Q99536	Synaptic vesicle membrane protein VAT-1 homolog	VAT1	41,9	6,29	1,65
291	O00161	Synaptosomal-associated protein 23	SNAP23	23,3	5,01	runter
292	O95881	Thioredoxin domain-containing protein 12	TXNDC12	19,2	5,40	1,92
293	Q13769	THO complex subunit 5 homolog	THOC5	78,5	6,87	0,57
294	Q86W42	THO complex subunit 6 homolog	THOC6	37,5	7,43	0,31
295	P23919	Thymidylate kinase	DTYMK	23,8	8,27	0,58
296	Q15654	Thyroid receptor-interacting protein 6	TRIP6	50,3	7,37	0,56
297	Q07157	Tight junction protein ZO-1	TJP1	195,3	6,70	1,53
298	P46937	Transcriptional coactivator YAP1	YAP1	54,4	5,17	1,51
299	Q86YP4	Transcriptional repressor p66-alpha	GATAD2A	68,0	9,94	runter
300	P02786	Transferrin receptor protein 1	TFRC	84,8	6,61	0,58
301	Q9BTV4	Transmembrane protein 43	TMEM43	44,8	8,13	0,52
302	Q7Z2T5	TRMT1-like protein	TRMT1L	81,7	7,88	1,69
303	Q9Y606	tRNA pseudouridine synthase A, mitochondrial	PUS1	47,4	8,41	runter
304	P07951	Tropomyosin beta chain	TPM2	32,8	4,70	0,62
305	Q9BQE3	Tubulin alpha-1C chain	TUBA1C	49,9	5,10	1,96
306	Q13509	Tubulin beta-3 chain	TUBB3	50,4	4,93	2,08
307	P04350	Tubulin beta-4A chain	TUBB4A	49,6	4,88	5,10
308	Q9BUF5	Tubulin beta-6 chain	TUBB6	49,8	4,88	2,00
309	P23258	Tubulin gamma-1 chain	TUBG1	51,1	6,14	0,59
310	Q9NRH3	Tubulin gamma-2 chain	TUBG2	51,1	5,80	0,59
311	Q15813	Tubulin-specific chaperone E	TBCE	59,3	6,76	runter
312	Q14166	Tubulin--tyrosine ligase-like protein 12	TTLL12	74,4	5,53	0,56
313	P25445	Tumor necrosis factor receptor superfamily member 6	FAS	37,7	7,94	0,63
314	Q6IBS0	Twinfilin-2	TWF2	39,5	6,84	runter
315	P18031	Tyrosine-protein phosphatase non-receptor type 1	PTPN1	49,9	6,27	0,62
316	O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	244,4	6,06	1,66
317	Q9UMX0	Ubiquilin-1	UBQLN1	62,5	5,11	0,64
318	Q9Y4E8	Ubiquitin carboxyl-terminal hydrolase 15	USP15	112,3	5,22	runter
319	P45974	Ubiquitin carboxyl-terminal hydrolase 5	USP5	95,7	5,03	0,60
320	Q93009	Ubiquitin carboxyl-terminal hydrolase 7	USP7	128,2	5,55	0,25
321	O14562	Ubiquitin domain-containing protein UBFD1	UBFD1	33,4	5,77	0,64
322	P61086	Ubiquitin-conjugating enzyme E2 K	UBE2K	22,4	5,44	1,51
323	Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1	UGGT1	177,1	5,63	2,16
324	Q16222	UDP-N-acetylhexosamine pyrophosphorylase	UAP1	58,7	6,33	2,06
325	P54727	UV excision repair protein RAD23 homolog B	RAD23B	43,1	4,84	0,59
326	P50552	Vasodilator-stimulated phosphoprotein	VASP	39,8	8,94	0,65

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327	Q9P035	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3	HACD3	43,1	8,94	1,52
328	O75396	Vesicle-trafficking protein SEC22b	SEC22B	24,6	6,92	1,52
329	P12955	Xaa-Pro dipeptidase	PD	54,5	6,00	0,61
330	Q96ME7	Zinc finger protein 512	ZNF512	64,6	9,76	runter
331	O75312	Zinc finger protein ZPR1	ZPR1	50,9	4,73	runter

Tabelle S3: Differenziell exprimierte Proteine von transient transfizierten HEK-293 Zellen bei 20 µM Methionin (mock *vs*. NNMT)

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
1	Q9C0C2	182 kDa tankyrase-1-binding protein	TNKS1BP1	181,7	4,86	0,60
2	O00232	26S proteasome non-ATPase regulatory subunit 12	PSMD12	52,9	7,65	1,71
3	Q9Y676	28S ribosomal protein S18b, mitochondrial	MRPS18B	29,4	9,38	0,60
4	P82650	28S ribosomal protein S22, mitochondrial	MRPS22	41,3	7,90	0,53
5	P12694	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	BCKDHA	50,4	8,27	runter
6	Q13405	39S ribosomal protein L49, mitochondrial	MRPL49	19,2	9,45	runter
7	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial	HIBADH	35,3	8,13	runter
8	P62277	40S ribosomal protein S13	RPS13	17,2	10,54	0,38
9	P62841	40S ribosomal protein S15	RPS15	17,0	10,39	0,54
10	P62244	40S ribosomal protein S15a	RPS15A	14,8	10,13	0,62
11	P62249	40S ribosomal protein S16	RPS16	16,4	10,21	0,64
12	P62269	40S ribosomal protein S18	RPS18	17,7	10,99	0,66
13	P63220	40S ribosomal protein S21	RPS21	9,1	8,50	0,53
14	P23396	40S ribosomal protein S3	RPS3	26,7	9,66	0,62
15	P22090	40S ribosomal protein S4, Y isoform 1	RPS4Y1	29,4	10,24	0,54
16	Q8TD47	40S ribosomal protein S4, Y isoform 2	RPS4Y2	29,3	10,08	0,56
17	P62906	60S ribosomal protein L10a	RPL10A	24,8	9,94	0,62
18	P62913	60S ribosomal protein L11	RPL11	20,2	9,60	0,49
19	Q07020	60S ribosomal protein L18	RPL18	21,6	11,72	0,64
20	P62750	60S ribosomal protein L23a	RPL23A	17,7	10,45	0,53
21	P83731	60S ribosomal protein L24	RPL24	17,8	11,25	0,57
22	P61254	60S ribosomal protein L26	RPL26	17,2	10,55	0,59
23	Q9UNX3	60S ribosomal protein L26-like 1	RPL26L1	17,2	10,55	0,22
24	P46779	60S ribosomal protein L28	RPL28	15,7	12,02	3,64
25	P24752	Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	45,2	8,85	0,58
26	Q99798	Aconitate hydratase, mitochondrial	ACO2	85,4	7,61	1,50
27	Q92747	Actin-related protein 2/3 complex subunit 1A	ARPC1A	41,5	8,18	3,81

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
28	O95433	Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	38,3	5,53	1,67
29	Q9H845	Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	68,7	7,96	0,33
30	P07108	Acyl-CoA-binding protein	DBI	10,0	6,57	0,52
31	P55263	Adenosine kinase	ADK	40,5	6,70	1,70
32	P84077	ADP-ribosylation factor 1	ARF1	20,7	6,80	0,52
33	P61204	ADP-ribosylation factor 3	ARF3	20,6	7,43	0,52
34	Q9UKK9	ADP-sugar pyrophosphatase	NUDT5	24,3	4,94	1,76
35	Q9NRG9	Aladin	AAAS	59,5	7,50	hoch
36	P30837	Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	57,2	6,80	4,96
37	O43768	Alpha-endosulfine	ENSA	13,4	7,24	0,51
38	P12429	Annexin A3	ANXA3	36,4	5,92	1,80
39	P20073	Annexin A7	ANXA7	52,7	5,68	1,54
40	O14617	AP-3 complex subunit delta-1	AP3D1	130,1	8,48	0,56
41	Q07812	Apoptosis regulator BAX	BAX	21,2	5,22	runter
42	Q9UBB4	Ataxin-10	ATXN10	53,5	5,25	0,61
43	O75947	ATP synthase subunit d, mitochondrial	ATP5H	18,5	5,30	0,63
44	P18859	ATP synthase-coupling factor 6, mitochondrial	ATP5J	12,6	9,52	0,65
45	P28288	ATP-binding cassette sub-family D member 3	ABCD3	75,4	9,36	1,93
46	P17858	ATP-dependent 6-phosphofructokinase, liver type	PFKL	85,0	7,50	1,63
47	Q9NUU7	ATP-dependent RNA helicase DDX19A	DDX19A	53,9	6,58	0,66
48	Q9UMR2	ATP-dependent RNA helicase DDX19B	DDX19B	53,9	6,30	0,58
49	O00148	ATP-dependent RNA helicase DDX39A	DDX39A	49,1	5,68	hoch
50	O75531	Barrier-to-autointegration factor	BANF1	10,1	6,09	0,47
51	Q9Y6E2	Basic leucine zipper and W2 domain-containing protein 2	BZW2	48,1	6,68	runter
52	P55957	BH3-interacting domain death agonist	BID	22,0	5,44	0,65
53	O95340	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2	PAPSS2	69,5	8,03	runter
54	Q13867	Bleomycin hydrolase	BLMH	52,5	6,27	2,22
55	O15382	Branched-chain-amino-acid aminotransferase, mitochondrial	BCAT2	44,3	8,65	runter
56	P19022	Cadherin-2	CDH2	99,7	4,81	runter
57	Q8IWX8	Calcium homeostasis endoplasmic reticulum protein	CHERP	103,6	9,04	5,42
58	Q6NUK1	Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	53,3	6,33	3,22
59	P04632	Calpain small subunit 1	CAPNS1	28,3	5,20	0,56
60	P20810	Calpastatin	CAST	76,5	5,07	0,66
61	Q96DG6	Carboxymethylenebutenolidase homolog	CMBL	28,0	7,18	0,48
62	P67870	Casein kinase II subunit beta	CSNK2B	24,9	5,55	1,90
63	P42574	Caspase-3	CASP3	31,6	6,54	0,38
64	O60716	Catenin delta-1	CTNND1	108,1	6,23	0,62

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
65	P07339	Cathepsin D	CTSD	44,5	6,54	0,66
66	P11717	Cation-independent mannose-6-phosphate receptor	IGF2R	274,2	5,94	2,02
67	Q5ZPR3	CD276 antigen	CD276	57,2	4,91	2,02
68	P13987	CD59 glycoprotein	CD59	14,2	6,48	0,63
69	P60953	Cell division control protein 42 homolog	CDC42	21,2	6,55	0,62
70	Q8IXM2	Chromatin complexes subunit BAP18	BAP18	17,9	7,33	0,63
71	P09496	Clathrin light chain A	CLTA	27,1	4,51	0,57
72	O43809	Cleavage and polyadenylation specificity factor subunit 5	NUDT21	26,2	8,82	0,27
73	Q9H0L4	Cleavage stimulation factor subunit 2 tau variant	CSTF2T	64,4	7,25	0,58
74	Q12996	Cleavage stimulation factor subunit 3	CSTF3	82,9	8,12	1,66
75	P35606	Coatomer subunit beta'	COPB2	102,4	5,27	1,56
76	P23528	Cofilin-1	CFL1	18,5	8,09	0,66
77	Q92905	COP9 signalosome complex subunit 5	COPS5	37,6	6,54	0,63
78	Q13363	C-terminal-binding protein 1	CTBP1	47,5	6,77	1,91
79	Q92879	CUGBP Elav-like family member 1	CELF1	52,0	8,46	0,53
80	Q13617	Cullin-2	CUL2	86,9	6,92	1,59
81	P10606	Cytochrome c oxidase subunit 5B, mitochondrial	COX5B	13,7	8,81	0,54
82	P14854	Cytochrome c oxidase subunit 6B1	COX6B1	10,2	7,05	0,56
83	P21399	Cytoplasmic aconitate hydratase	ACO1	98,3	6,68	1,57
84	O43175	D-3-phosphoglycerate dehydrogenase	PHGDH	56,6	6,71	0,63
85	Q96HY6	DDRGK domain-containing protein 1	DDRGK1	35,6	5,12	0,29
86	P36957	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	DLST	48,7	8,95	1,83
87	Q9BPU6	Dihydropyrimidinase-related protein 5	DPYSL5	61,4	7,20	0,63
88	P49642	DNA primase small subunit	PRIM1	49,9	8,21	2,46
89	P25685	DnaJ homolog subfamily B member 1	DNAJB1	38,0	8,63	0,59
90	Q99543	DnaJ homolog subfamily C member 2	DNAJC2	72,0	8,70	runter
91	Q99615	DnaJ homolog subfamily C member 7	DNAJC7	56,4	6,96	1,68
92	O75937	DnaJ homolog subfamily C member 8	DNAJC8	29,8	9,06	0,46
93	Q14203	Dynactin subunit 1	DCTN1	141,6	5,81	2,11
94	Q9UJW0	Dynactin subunit 4	DCTN4	52,3	7,34	0,53
95	O60313	Dynamin-like 120 kDa protein, mitochondrial	OPA1	111,6	7,87	runter
96	P63167	Dynein light chain 1, cytoplasmic	DYNLL1	10,4	7,40	0,50
97	Q99496	E3 ubiquitin-protein ligase RING2	RNF2	37,6	6,84	runter
98	Q96C19	EF-hand domain-containing protein D2	EFHD2	26,7	5,20	21,40
99	P13804	Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	35,1	8,38	0,60
100	O75477	Erlin-1	ERLIN1	38,9	7,87	1,94
101	P30042	ES1 protein homolog, mitochondrial	C21orf33	28,2	8,27	1,89

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
102	P38919	Eukaryotic initiation factor 4A-III	EIF4A3	46,8	6,73	1,58
103	O43324	Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	19,8	8,54	runter
104	P41567	Eukaryotic translation initiation factor 1	EIF1	12,7	7,44	0,63
105	P55884	Eukaryotic translation initiation factor 3 subunit B	EIF3B	92,4	5,00	1,56
106	O15372	Eukaryotic translation initiation factor 3 subunit H	EIF3H	39,9	6,54	0,25
107	P23588	Eukaryotic translation initiation factor 4B	EIF4B	69,1	5,73	0,64
108	Q15056	Eukaryotic translation initiation factor 4H	EIF4H	27,4	7,23	0,53
109	O43592	Exportin-T	XPOT	109,9	5,39	1,63
110	P14324	Farnesyl pyrophosphate synthase	FDPS	48,2	6,15	hoch
111	Q96CS3	FAS-associated factor 2	FAF2	52,6	5,62	1,80
112	Q01469	Fatty acid-binding protein, epidermal	FABP5	15,2	7,01	0,63
113	Q96AC1	Fermitin family homolog 2	FERMT2	77,8	6,70	hoch
114	Q96CP2	FLYWCH family member 2	FLYWCH2	14,6	8,46	0,63
115	P51570	Galactokinase	GALK1	42,2	6,46	0,62
116	O94766	Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3	B3GAT3	37,1	8,27	hoch
117	P09382	Galectin-1	LGALS1	14,7	5,50	0,59
118	P35269	General transcription factor IIF subunit 1	GTF2F1	58,2	7,49	runter
119	P47897	Glutamine--tRNA ligase	QARS	87,7	7,15	1,81
120	Q92947	Glutaryl-CoA dehydrogenase, mitochondrial	GCDH	48,1	8,06	runter
121	P28161	Glutathione S-transferase Mu 2	GSTM2	25,7	6,37	runter
122	Q9H4A6	Golgi phosphoprotein 3	GOLPH3	33,8	6,44	2,91
123	Q9H8Y8	Golgi reassembly-stacking protein 2	GORASP2	47,1	4,82	0,64
124	Q86YR5	G-protein-signaling modulator 1	GPSM1	74,5	6,54	1,50
125	Q12849	G-rich sequence factor 1	GRSF1	53,1	6,19	0,45
126	P63092	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	GNAS	45,6	5,82	1,63
127	Q5JWF2	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	111,0	5,03	1,63
128	P04792	Heat shock protein beta-1	HSPB1	22,8	6,40	0,56
129	P51858	Hepatoma-derived growth factor	HDGF	26,8	4,73	0,56
130	Q7Z4V5	Hepatoma-derived growth factor-related protein 2	HDGFRP2	74,3	7,49	0,55
131	P09429	High mobility group protein B1	HMGB1	24,9	5,74	0,57
132	Q92769	Histone deacetylase 2	HDAC2	55,3	5,91	0,64
133	Q92522	Histone H1x	H1FX	22,5	10,76	0,66
134	Q71DI3	Histone H3.2	HIST2H3A	15,4	11,27	0,58
135	P84243	Histone H3.3	H3F3A	15,3	11,27	1,51
136	Q9NZL4	Hsp70-binding protein 1	HSPBP1	39,4	5,21	hoch

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
137	O60684	Importin subunit alpha-7	KPNA6	60,0	4,98	hoch
138	O00410	Importin-5	IPO5	123,6	4,94	1,51
139	Q7Z5L9	Interferon regulatory factor 2-binding protein 2	IRF2BP2	61,0	8,69	0,66
140	O43837	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	42,2	8,46	1,57
141	Q9Y624	Junctional adhesion molecule A	F11R	32,6	7,90	2,20
142	Q7Z4H8	KDEL motif-containing protein 2	KDELC2	58,5	8,24	2,32
143	Q9NSK0	Kinesin light chain 4	KLC4	68,6	6,18	0,65
144	Q14696	LDLR chaperone MESD	MESDC2	26,1	7,78	0,60
145	O95202	LETM1 and EF-hand domain-containing protein 1, mitochondrial	LETM1	83,3	6,70	1,71
146	P30740	Leukocyte elastase inhibitor	SERPINB1	42,7	6,28	runter
147	O95573	Long-chain-fatty-acid--CoA ligase 3	ACSL3	80,4	8,38	2,02
148	P56192	Methionine--tRNA ligase, cytoplasmic	MARS	101,1	6,16	1,59
149	Q9NX63	MIC complex subunit MIC19	CHCHD3	26,1	8,28	0,49
150	P55081	Microfibrillar-associated protein 1	MFAP1	51,9	4,98	0,59
151	P46821	Microtubule-associated protein 1B	MAP1B	270,5	4,81	runter
152	P21741	Midkine	MDK	15,6	9,79	0,60
153	P27361	Mitogen-activated protein kinase 3	MAPK3	43,1	6,74	hoch
154	Q96T76	MMS19 nucleotide excision repair protein homolog	MMS19	113,2	6,35	runter
155	Q9Y3A3	MOB-like protein phocein	MOB4	26,0	5,78	hoch
156	O95865	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	DDAH2	29,6	6,01	runter
157	P23368	NAD-dependent malic enzyme, mitochondrial	ME2	65,4	7,61	hoch
158	P48163	NADP-dependent malic enzyme	ME1	64,1	6,13	hoch
159	P22570	NADPH:adrenodoxin oxidoreductase, mitochondrial	FDXR	53,8	8,44	0,48
160	P41227	N-alpha-acetyltransferase 10	NAA10	26,4	5,64	1,51
161	Q9GZZ1	N-alpha-acetyltransferase 50	NAA50	19,4	8,81	0,66
162	Q8TBC4	NEDD8-activating enzyme E1 catalytic subunit	UBA3	51,8	5,45	0,43
163	P61081	NEDD8-conjugating enzyme Ubc12	UBE2M	20,9	7,69	0,61
164	Q8WX92	Negative elongation factor B	NELFB	65,7	6,13	hoch
165	Q96TA1	Niban-like protein 1	FAM129B	84,1	6,19	2,53
166	**P40261**	**Nicotinamide N-methyltransferase**	**NNMT**	**29,6**	**5,74**	**hoch**
167	Q15155	Nodal modulator 1	NOMO1	134,2	5,81	1,70
168	Q5JPE7	Nodal modulator 2	NOMO2	139,4	5,76	1,70
169	P69849	Nodal modulator 3	NOMO3	134,0	5,67	1,70
170	P57740	Nuclear pore complex protein Nup107	NUP107	106,3	5,43	0,51
171	Q9UKX7	Nuclear pore complex protein Nup50	NUP50	50,1	7,06	0,54
172	P52948	Nuclear pore complex protein Nup98-Nup96	NUP98	197,5	6,40	0,59
173	Q9HCD5	Nuclear receptor coactivator 5	NCOA5	65,5	9,60	0,60

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
174	Q14978	Nucleolar and coiled-body phosphoprotein 1	NOLC1	73,6	9,47	0,63
175	Q9Y3B8	Oligoribonuclease, mitochondrial	REXO2	26,8	6,87	0,62
176	P04181	Ornithine aminotransferase, mitochondrial	OAT	48,5	7,03	1,62
177	Q8WX93	Palladin	PALLD	150,5	7,09	runter
178	O75475	PC4 and SFRS1-interacting protein	PSIP1	60,1	9,13	0,50
179	Q53GG5	PDZ and LIM domain protein 3	PDLIM3	39,2	6,89	0,66
180	P26885	Peptidyl-prolyl cis-trans isomerase FKBP2	FKBP2	15,6	9,13	0,66
181	Q9Y237	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	PIN4	13,8	9,77	0,42
182	P48739	Phosphatidylinositol transfer protein beta isoform	PITPNB	31,5	6,87	1,52
183	Q9BY77	Polymerase delta-interacting protein 3	POLDIP3	46,1	9,99	0,66
184	Q8TCS8	Polyribonucleotide nucleotidyltransferase 1, mitochondrial	PNPT1	85,9	7,77	hoch
185	Q9UHG3	Prenylcysteine oxidase 1	PCYOX1	56,6	6,18	2,15
186	Q8IY81	pre-rRNA processing protein FTSJ3	FTSJ3	96,5	8,40	0,59
187	Q7L014	Probable ATP-dependent RNA helicase DDX46	DDX46	117,3	9,29	2,14
188	P07737	Profilin-1	PFN1	15,0	8,27	0,66
189	Q53EL6	Programmed cell death protein 4	PDCD4	51,7	5,21	0,47
190	P35232	Prohibitin	PHB	29,8	5,76	runter
191	Q14914	Prostaglandin reductase 1	PTGR1	35,8	8,29	0,50
192	P49721	Proteasome subunit beta type-2	PSMB2	22,8	7,02	runter
193	Q99873	Protein arginine N-methyltransferase 1	PRMT1	41,5	5,43	1,76
194	O00622	Protein CYR61	CYR61	42,0	8,21	2,35
195	Q8NCA5	Protein FAM98A	FAM98A	55,4	9,03	1,56
196	Q9UGV2	Protein NDRG3	NDRG3	41,4	5,31	1,50
197	Q96C90	Protein phosphatase 1 regulatory subunit 14B	PPP1R14B	15,9	4,86	0,46
198	Q15435	Protein phosphatase 1 regulatory subunit 7	PPP1R7	41,5	4,91	0,63
199	Q96PU8	Protein quaking	QKI	37,6	8,56	runter
200	P31949	Protein S100-A11	S100A11	11,7	7,12	runter
201	Q14671	Pumilio homolog 1	PUM1	126,4	6,84	runter
202	Q9HCE1	Putative helicase MOV-10	MOV10	113,6	8,82	2,54
203	B2RPK0	Putative high mobility group protein B1-like 1	HMGB1P1	24,2	6,21	0,52
204	O60361	Putative nucleoside diphosphate kinase	NME2P1	15,5	8,57	1,55
205	Q49A26	Putative oxidoreductase GLYR1	GLYR1	60,5	9,17	runter
206	Q9NVS9	Pyridoxine-5'-phosphate oxidase	PNPO	30,0	7,06	1,63
207	P11177	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	39,2	6,65	0,66
208	O00330	Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	54,1	8,66	0,66
209	P62491	Ras-related protein Rab-11A	RAB11A	24,4	6,57	0,34
210	Q15907	Ras-related protein Rab-11B	RAB11B	24,5	5,94	0,34

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
211	P51149	Ras-related protein Rab-7a	RAB7A	23,5	6,70	0,65
212	P61006	Ras-related protein Rab-8A	RAB8A	23,7	9,07	0,34
213	Q96DB5	Regulator of microtubule dynamics protein 1	RMDN1	35,8	8,50	hoch
214	P23921	Ribonucleoside-diphosphate reductase large subunit	RRM1	90,0	7,15	0,40
215	Q9Y4W2	Ribosomal biogenesis protein LAS1L	LAS1L	83,0	4,73	1,57
216	Q9H7B2	Ribosome production factor 2 homolog	RPF2	35,6	9,99	hoch
217	P98179	RNA-binding protein 3	RBM3	17,2	8,91	0,47
218	P22087	rRNA 2'-O-methyltransferase fibrillarin	FBL	33,8	10,18	0,56
219	Q5JTH9	RRP12-like protein	RRP12	143,6	8,75	1,52
220	Q15424	Scaffold attachment factor B1	SAFB	102,6	5,47	0,59
221	P49903	Selenide, water dikinase 1	SEPHS1	42,9	5,97	0,49
222	Q13247	Serine/arginine-rich splicing factor 6	SRSF6	39,6	11,43	0,31
223	Q16629	Serine/arginine-rich splicing factor 7	SRSF7	27,4	11,82	4,09
224	P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	PPP2R2A	51,7	6,20	0,53
225	Q9Y5M8	Signal recognition particle receptor subunit beta	SRPRB	29,7	9,04	0,57
226	O76094	Signal recognition particle subunit SRP72	SRP72	74,6	9,26	2,03
227	Q92783	Signal transducing adapter molecule 1	STAM	59,1	4,82	runter
228	Q13573	SNW domain-containing protein 1	SNW1	61,5	9,52	runter
229	P30626	Sorcin	SRI	21,7	5,59	0,59
230	O60493	Sorting nexin-3	SNX3	18,8	8,66	0,38
231	Q8N0X7	Spartin	SPG20	72,8	5,91	0,61
232	Q15020	Squamous cell carcinoma antigen recognized by T-cells 3	SART3	109,9	5,57	1,50
233	P35610	Sterol O-acyltransferase 1	SOAT1	64,7	8,94	1,61
234	Q9UJZ1	Stomatin-like protein 2, mitochondrial	STOML2	38,5	7,39	0,53
235	O95347	Structural maintenance of chromosomes protein 2	SMC2	135,6	8,43	0,43
236	P63279	SUMO-conjugating enzyme UBC9	UBE2I	18,0	8,66	0,46
237	P42285	Superkiller viralicidic activity 2-like 2	SKIV2L2	117,7	6,52	0,53
238	Q969G3	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	SMARCE1	46,6	4,88	8,26
239	O00161	Synaptosomal-associated protein 23	SNAP23	23,3	5,01	0,55
240	P0CG34	Thymosin beta-15A	TMSB15A	5,2	5,36	0,59
241	P62328	Thymosin beta-4	TMSB4X	5,1	5,06	0,51
242	O75663	TIP41-like protein	TIPRL	31,4	5,91	0,57
243	Q86YP4	Transcriptional repressor p66-alpha	GATAD2A	68,0	9,94	runter
244	P02786	Transferrin receptor protein 1	TFRC	84,8	6,61	1,55
245	Q99598	Translin-associated protein X	TSNAX	33,1	6,55	1,56
246	Q92544	Transmembrane 9 superfamily member 4	TM9SF4	74,5	6,54	0,36

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
247	Q9BTV4	Transmembrane protein 43	TMEM43	44,8	8,13	runter
248	P55084	Trifunctional enzyme subunit beta, mitochondrial	HADHB	51,3	9,41	0,64
249	Q3LXA3	Triokinase/FMN cyclase	TKFC	58,9	7,49	runter
250	P29144	Tripeptidyl-peptidase 2	TPP2	138,3	6,32	1,97
251	Q7Z2T5	TRMT1-like protein	TRMT1L	81,7	7,88	2,95
252	P04350	Tubulin beta-4A chain	TUBB4A	49,6	4,88	2,33
253	P68371	Tubulin beta-4B chain	TUBB4B	49,8	4,89	10,95
254	O75347	Tubulin-specific chaperone A	TBCA	12,8	5,29	0,65
255	Q16890	Tumor protein D53	TPD52L1	22,4	5,62	0,65
256	Q9Y2Z4	Tyrosine--tRNA ligase, mitochondrial	YARS2	53,2	8,98	runter
257	O43172	U4/U6 small nuclear ribonucleoprotein Prp4	PRPF4	58,4	7,42	0,28
258	Q9UMX0	Ubiquilin-1	UBQLN1	62,5	5,11	0,63
259	Q14694	Ubiquitin carboxyl-terminal hydrolase 10	USP10	87,1	5,31	0,59
260	Q93009	Ubiquitin carboxyl-terminal hydrolase 7	USP7	128,2	5,55	1,56
261	Q9Y5K5	Ubiquitin carboxyl-terminal hydrolase isozyme L5	UCHL5	37,6	5,33	2,11
262	Q92890	Ubiquitin fusion degradation protein 1 homolog	UFD1L	34,5	6,70	0,65
263	Q13404	Ubiquitin-conjugating enzyme E2 variant 1	UBE2V1	16,5	7,93	0,40
264	Q9GZZ9	Ubiquitin-like modifier-activating enzyme 5	UBA5	44,8	4,84	0,54
265	Q9HB07	UPF0160 protein MYG1, mitochondrial	C12orf10	42,4	6,67	runter
266	P54725	UV excision repair protein RAD23 homolog A	RAD23A	39,6	4,58	runter
267	O75351	Vacuolar protein sorting-associated protein 4B	VPS4B	49,3	7,23	runter
268	Q9P0L0	Vesicle-associated membrane protein-associated protein A	VAPA	27,9	8,62	0,59
269	P46459	Vesicle-fusing ATPase	NSF	82,5	6,95	1,68
270	O75396	Vesicle-trafficking protein SEC22b	SEC22B	24,6	6,92	2,21
271	P38606	V-type proton ATPase catalytic subunit A	ATP6V1A	68,3	5,52	1,81
272	Q9UI12	V-type proton ATPase subunit H	ATP6V1H	55,8	6,48	3,19
273	P12955	Xaa-Pro dipeptidase	PD	54,5	6,00	1,72
274	O15231	Zinc finger protein 185	ZNF185	73,5	7,01	0,38

Tabelle S4: Differenziell exprimierte Proteine von transient transfizierten Caki-1 Zellen bei 100 µM Methionin (sisc *vs*. siNNMT)

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs*. siNNMT
1	Q15029	116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	109,4	5,00	0,44
2	Q16698	2,4-dienoyl-CoA reductase, mitochondrial	DECR1	36,0	9,28	0,31
3	P62191	26S protease regulatory subunit 4	PSMC1	49,2	6,21	1,53

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs*. siNNMT
4	P62195	26S protease regulatory subunit 8	PSMC5	45,6	7,55	2,45
5	Q99460	26S proteasome non-ATPase regulatory subunit 1	PSMD1	105,8	5,39	1,68
6	O43242	26S proteasome non-ATPase regulatory subunit 3	PSMD3	60,9	8,44	0,59
7	Q9Y676	28S ribosomal protein S18b, mitochondrial	MRPS18B	29,4	9,38	0,46
8	P51398	28S ribosomal protein S29, mitochondrial	DAP3	45,5	8,88	0,54
9	Q9NP92	28S ribosomal protein S30, mitochondrial	MRPS30	50,3	7,97	0,66
10	Q92665	28S ribosomal protein S31, mitochondrial	MRPS31	45,3	9,29	1,79
11	Q9Y2R9	28S ribosomal protein S7, mitochondrial	MRPS7	28,1	9,99	2,07
12	O95861	3'(2'),5'-bisphosphate nucleotidase 1	BPNT1	33,4	5,69	0,56
13	Q9BYD6	39S ribosomal protein L1, mitochondrial	MRPL1	36,9	8,78	1,59
14	Q13405	39S ribosomal protein L49, mitochondrial	MRPL49	19,2	9,45	1,67
15	P62841	40S ribosomal protein S15	RPS15	17,0	10,39	3,18
16	P62244	40S ribosomal protein S15a	RPS15A	14,8	10,13	0,59
17	P62266	40S ribosomal protein S23	RPS23	15,8	10,49	1,76
18	P23396	40S ribosomal protein S3	RPS3	26,7	9,66	0,42
19	P62241	40S ribosomal protein S8	RPS8	24,2	10,32	0,60
20	Q9BRK5	45 kDa calcium-binding protein	SDF4	41,8	4,86	2,10
21	P08195	4F2 cell-surface antigen heavy chain	SLC3A2	68,0	5,01	0,36
22	P49189	4-trimethylaminobutyraldehyde dehydrogenase	ALDH9A1	53,8	5,87	2,73
23	P05387	60S acidic ribosomal protein P2	RPLP2	11,7	4,54	1,54
24	P62906	60S ribosomal protein L10a	RPL10A	24,8	9,94	0,62
25	P40429	60S ribosomal protein L13a	RPL13A	23,6	10,93	0,44
26	P61313	60S ribosomal protein L15	RPL15	24,1	11,62	0,59
27	Q07020	60S ribosomal protein L18	RPL18	21,6	11,72	0,51
28	P84098	60S ribosomal protein L19	RPL19	23,5	11,47	0,64
29	P62750	60S ribosomal protein L23a	RPL23A	17,7	10,45	2,90
30	P61254	60S ribosomal protein L26	RPL26	17,2	10,55	1,88
31	Q9UNX3	60S ribosomal protein L26-like 1	RPL26L1	17,2	10,55	2,16
32	P46779	60S ribosomal protein L28	RPL28	15,7	12,02	10,02
33	P39023	60S ribosomal protein L3	RPL3	46,1	10,18	0,64
34	P36578	60S ribosomal protein L4	RPL4	47,7	11,06	0,62
35	P18124	60S ribosomal protein L7	RPL7	29,2	10,65	0,61
36	Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic	ACAT2	41,3	6,92	hoch
37	P24752	Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	45,2	8,85	0,59
38	Q13510	Acid ceramidase	ASAH1	44,6	7,62	1,80
39	Q9BTT0	Acidic leucine-rich nuclear phosphoprotein 32 family member E	ANP32E	30,7	3,85	0,52
40	P53999	Activated RNA polymerase II transcriptional coactivator p15	SUB1	14,4	9,60	1,82

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs*. siNNMT
41	Q86TX2	Acyl-coenzyme A thioesterase 1	ACOT1	46,2	7,34	hoch
42	P49753	Acyl-coenzyme A thioesterase 2, mitochondrial	ACOT2	53,2	8,47	hoch
43	Q9Y305	Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	49,9	8,60	1,78
44	P46108	Adapter molecule crk	CRK	33,8	5,55	0,65
45	P07741	Adenine phosphoribosyltransferase	APRT	19,6	6,02	runter
46	O43865	Adenosylhomocysteinase 2	AHCYL1	58,9	6,89	1,93
47	P40123	Adenylyl cyclase-associated protein 2	CAP2	52,8	6,37	hoch
48	Q9HDC9	Adipocyte plasma membrane-associated protein	APMAP	46,5	6,16	1,58
49	P12235	ADP/ATP translocase 1	SLC25A4	33,0	9,76	runter
50	P05141	ADP/ATP translocase 2	SLC25A5	32,8	9,69	runter
51	P12236	ADP/ATP translocase 3	SLC25A6	32,8	9,74	runter
52	P84077	ADP-ribosylation factor 1	ARF1	20,7	6,80	0,59
53	P61204	ADP-ribosylation factor 3	ARF3	20,6	7,43	0,59
54	P62330	ADP-ribosylation factor 6	ARF6	20,1	8,95	0,62
55	Q8N6H7	ADP-ribosylation factor GTPase-activating protein 2	ARFGAP2	56,7	7,99	1,58
56	P30837	Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	57,2	6,80	7,66
57	P15121	Aldose reductase	AKR1B1	35,8	6,98	1,92
58	P30533	Alpha-2-macroglobulin receptor-associated protein	LRPAP1	41,4	8,78	1,69
59	Q9UHK6	Alpha-methylacyl-CoA racemase	AMACR	42,4	6,44	runter
60	P37840	Alpha-synuclein	SNCA	14,5	4,70	1,55
61	P15144	Aminopeptidase N	ANP	109,5	5,48	0,55
62	Q06481	Amyloid-like protein 2	APLP2	86,9	4,79	2,16
63	Q6FI81	Anamorsin	CIAPIN1	33,6	5,62	runter
64	Q9P0K7	Ankycorbin	RAI14	110,0	6,21	1,79
65	O94973	AP-2 complex subunit alpha-2	AP2A2	103,9	6,96	0,59
66	Q9BQE5	Apolipoprotein L2	APOL2	37,1	6,74	1,55
67	Q9BZZ5	Apoptosis inhibitor 5	API5	59,0	7,34	0,33
68	P00966	Argininosuccinate synthase	ASS1	46,5	8,02	runter
69	P08243	Asparagine synthetase [glutamine-hydrolyzing]	ASNS	64,3	6,86	runter
70	Q12797	Aspartyl/asparaginyl beta-hydroxylase	ASPH	85,8	5,01	0,64
71	Q9NVI7	ATPase family AAA domain-containing protein 3A	ATAD3A	71,3	8,98	2,29
72	Q5T2N8	ATPase family AAA domain-containing protein 3C	ATAD3C	46,4	9,31	hoch
73	Q8NE71	ATP-binding cassette sub-family F member 1	ABCF1	95,9	6,80	1,61
74	P53396	ATP-citrate synthase	ACLY	120,8	7,33	1,81
75	P08237	ATP-dependent 6-phosphofructokinase, muscle type	PFKM	85,1	7,99	2,15
76	Q08211	ATP-dependent RNA helicase A	DHX9	140,9	6,84	0,59
77	O95816	BAG family molecular chaperone regulator 2	BAG2	23,8	6,70	2,15

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs*. siNNMT
78	O95817	BAG family molecular chaperone regulator 3	BAG3	61,6	6,95	1,52
79	Q9Y6E2	Basic leucine zipper and W2 domain-containing protein 2	BZW2	48,1	6,68	0,65
80	P61769	Beta-2-microglobulin	B2M	13,7	6,52	2,42
81	Q562R1	Beta-actin-like protein 2	ACTBL2	42,0	5,59	0,04
82	O95340	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2	PAPSS2	69,5	8,03	0,35
83	Q13867	Bleomycin hydrolase	BLMH	52,5	6,27	hoch
84	P80723	Brain acid soluble protein 1	BASP1	22,7	4,63	1,75
85	P19022	Cadherin-2	CDH2	99,7	4,81	0,65
86	Q8NE86	Calcium uniporter protein, mitochondrial	MCU	39,8	8,65	runter
87	Q13557	Calcium/calmodulin-dependent protein kinase type II subunit delta	CAMK2D	56,3	7,25	1,57
88	Q05682	Caldesmon	CALD1	93,2	5,66	3,71
89	P27824	Calnexin	CANX	67,5	4,60	0,61
90	P07384	Calpain-1 catalytic subunit	CAPN1	81,8	5,67	0,54
91	P17655	Calpain-2 catalytic subunit	CAPN2	79,9	4,98	0,45
92	Q99439	Calponin-2	CNN2	33,7	7,33	1,89
93	Q15417	Calponin-3	CNN3	36,4	6,05	3,15
94	Q9BSD7	Cancer-related nucleoside-triphosphatase	NTPCR	20,7	9,54	runter
95	P30622	CAP-Gly domain-containing linker protein 1	CLIP1	162,1	5,36	runter
96	Q14444	Caprin-1	CAPRIN1	78,3	5,25	1,87
97	P07451	Carbonic anhydrase 3	CA3	29,5	7,34	1,57
98	O75718	Cartilage-associated protein	CRTAP	46,5	5,73	0,52
99	Q14790	Caspase-8	CASP8	55,4	5,10	1,92
100	P20645	Cation-dependent mannose-6-phosphate receptor	M6PR	31,0	5,83	hoch
101	Q6YHK3	CD109 antigen	CD109	161,6	5,85	1,51
102	Q5ZPR3	CD276 antigen	CD276	57,2	4,91	2,62
103	Q9Y696	Chloride intracellular channel protein 4	CLIC4	28,8	5,59	0,59
104	Q00610	Clathrin heavy chain 1	CLTC	191,5	5,69	0,52
105	P53675	Clathrin heavy chain 2	CLTCL1	186,9	5,85	0,66
106	Q14677	Clathrin interactor 1	CLINT1	68,2	6,42	1,73
107	O43809	Cleavage and polyadenylation specificity factor subunit 5	NUDT21	26,2	8,82	0,55
108	O96005	Cleft lip and palate transmembrane protein 1	CLPTM1	76,0	6,30	runter
109	Q14019	Coactosin-like protein	COTL1	15,9	5,67	2,37
110	Q8IVM0	Coiled-coil domain-containing protein 50	CCDC50	35,8	6,65	1,71
111	Q07021	Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	31,3	4,84	0,66
112	O75131	Copine-3	CPNE3	60,1	5,85	1,76

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs*. siNNMT
113	O75367	Core histone macro-H2A.1	H2AFY	39,6	9,79	0,62
114	Q9P0M6	Core histone macro-H2A.2	H2AFY2	40,0	9,69	0,58
115	P46109	Crk-like protein	CRKL	33,8	6,74	1,53
116	Q13617	Cullin-2	CUL2	86,9	6,92	3,26
117	Q86VP6	Cullin-associated NEDD8-dissociated protein 1	CAND1	136,3	5,78	0,55
118	P49589	Cysteine--tRNA ligase, cytoplasmic	CARS	85,4	6,76	0,59
119	P22695	Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	48,4	8,63	0,64
120	Q14204	Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	532,1	6,40	0,51
121	O00154	Cytosolic acyl coenzyme A thioester hydrolase	ACOT7	41,8	8,54	1,60
122	O43175	D-3-phosphoglycerate dehydrogenase	PHGDH	56,6	6,71	0,34
123	Q96GG9	DCN1-like protein 1	DCUN1D1	30,1	5,34	0,57
124	Q9H773	dCTP pyrophosphatase 1	DCTPP1	18,7	5,03	0,59
125	Q96HY6	DDRGK domain-containing protein 1	DDRGK1	35,6	5,12	runter
126	Q9Y3Z3	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	72,2	7,14	3,46
127	P33316	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial	DUT	26,5	9,36	0,36
128	P10515	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT	69,0	7,84	1,92
129	Q9NY33	Dipeptidyl peptidase 3	DPP3	82,5	5,10	0,66
130	P27487	Dipeptidyl peptidase 4	DPP4	88,2	6,04	2,02
131	Q13443	Disintegrin and metalloproteinase domain-containing protein 9	ADAM9	90,5	7,52	hoch
132	Q12959	Disks large homolog 1	DLG1	100,4	5,76	1,54
133	Q9NRW3	DNA dC->dU-editing enzyme APOBEC-3C	APOBEC3C	22,8	7,59	1,54
134	Q92878	DNA repair protein RAD50	RAD50	153,8	6,89	5,28
135	P33993	DNA replication licensing factor MCM7	MCM7	81,3	6,46	hoch
136	P78527	DNA-dependent protein kinase catalytic subunit	PRKDC	468,8	7,12	0,38
137	O15446	DNA-directed RNA polymerase I subunit RPA34	CD3EAP	55,0	8,51	hoch
138	O60884	DnaJ homolog subfamily A member 2	DNAJA2	45,7	6,48	1,56
139	Q9NVH1	DnaJ homolog subfamily C member 11	DNAJC11	63,2	8,40	0,42
140	P04844	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	69,2	5,69	0,62
141	Q8TCJ2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	93,6	8,91	0,65
142	Q16643	Drebrin	DBN1	71,4	4,45	0,66
143	P36507	Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	44,4	6,55	hoch
144	Q13561	Dynactin subunit 2	DCTN2	44,2	5,21	1,65
145	P49792	E3 SUMO-protein ligase RanBP2	RANBP2	358,0	6,20	0,42
146	Q9NZN4	EH domain-containing protein 2	EHD2	61,1	6,46	0,64
147	Q9H223	EH domain-containing protein 4	EHD4	61,1	6,76	hoch

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs*. siNNMT
148	P38117	Electron transfer flavoprotein subunit beta	ETFB	27,8	8,10	0,54
149	P68104	Elongation factor 1-alpha 1	EEF1A1	50,1	9,01	1,51
150	Q05639	Elongation factor 1-alpha 2	EEF1A2	50,4	9,03	1,63
151	Q99961	Endophilin-A2	SH3GL1	41,5	5,43	2,07
152	P42126	Enoyl-CoA delta isomerase 1, mitochondrial	ECI1	32,8	8,54	0,43
153	P42566	Epidermal growth factor receptor substrate 15	EPS15	98,6	4,64	runter
154	O75477	Erlin-1	ERLIN1	38,9	7,87	0,59
155	P38919	Eukaryotic initiation factor 4A-III	EIF4A3	46,8	6,73	0,55
156	P62495	Eukaryotic peptide chain release factor subunit 1	ETF1	49,0	5,71	0,58
157	O00303	Eukaryotic translation initiation factor 3 subunit F	EIF3F	37,5	5,45	0,52
158	O75821	Eukaryotic translation initiation factor 3 subunit G	EIF3G	35,6	6,13	2,23
159	O15372	Eukaryotic translation initiation factor 3 subunit H	EIF3H	39,9	6,54	9,29
160	Q13347	Eukaryotic translation initiation factor 3 subunit I	EIF3I	36,5	5,64	1,51
161	P56537	Eukaryotic translation initiation factor 6	EIF6	26,6	4,68	0,59
162	O14980	Exportin-1	XPO1	123,3	6,06	0,54
163	P55060	Exportin-2	CSE1L	110,3	5,77	0,46
164	Q9UIA9	Exportin-7	XPO7	123,8	6,32	0,44
165	Q9Y5B9	FACT complex subunit SPT16	SUPT16H	119,8	5,66	0,64
166	Q96AC1	Fermitin family homolog 2	FERMT2	77,8	6,70	runter
167	P02794	Ferritin heavy chain	FTH1	21,2	5,55	1,56
168	Q53EP0	Fibronectin type III domain-containing protein 3B	FNDC3B	132,8	5,95	1,54
169	P23142	Fibulin-1	FBLN1	77,2	5,22	0,64
170	Q13642	Four and a half LIM domains protein 1	FHL1	36,2	8,97	runter
171	Q9UEY8	Gamma-adducin	ADD3	79,1	6,32	2,28
172	P57764	Gasdermin-D	GSDMD	52,8	5,08	1,63
173	P35269	General transcription factor IIF subunit 1	GTF2F1	58,2	7,49	hoch
174	P04062	Glucosylceramidase	GBA	59,7	7,61	1,64
175	P09211	Glutathione S-transferase P	GSTP1	23,3	5,64	0,62
176	P43304	Glycerol-3-phosphate dehydrogenase, mitochondrial	GPD2	80,8	7,69	1,95
177	Q9H8Y8	Golgi reassembly-stacking protein 2	GORASP2	47,1	4,82	1,65
178	Q99988	Growth/differentiation factor 15	GDF15	34,1	9,66	2,64
179	P04899	Guanine nucleotide-binding protein G(i) subunit alpha-2	GNAI2	40,4	5,54	0,60
180	P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	GNB1	37,4	6,00	0,64
181	P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	37,3	6,00	1,57
182	P08754	Guanine nucleotide-binding protein G(k) subunit alpha	GNAI3	40,5	5,69	0,55
183	P50148	Guanine nucleotide-binding protein G(q) subunit alpha	GNAQ	42,1	5,68	0,57

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs*. siNNMT
184	P63092	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	GNAS	45,6	5,82	2,02
185	Q5JWF2	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	111,0	5,03	2,02
186	Q14344	Guanine nucleotide-binding protein subunit alpha-13	GNA13	44,0	8,00	2,22
187	O43301	Heat shock 70 kDa protein 12A	HSPA12A	74,9	6,77	0,21
188	P34931	Heat shock 70 kDa protein 1-like	HSPA1L	70,3	6,02	1,64
189	O95757	Heat shock 70 kDa protein 4L	HSPA4L	94,5	5,88	hoch
190	Q92598	Heat shock protein 105 kDa	HSPH1	96,8	5,39	1,64
191	P04792	Heat shock protein beta-1	HSPB1	22,8	6,40	1,87
192	Q9NRV9	Heme-binding protein 1	HEBP1	21,1	5,80	1,55
193	O14964	Hepatocyte growth factor-regulated tyrosine kinase substrate	HGS	86,1	6,16	hoch
194	Q5SSJ5	Heterochromatin protein 1-binding protein 3	HP1BP3	61,2	9,67	0,59
195	O15347	High mobility group protein B3	HMGB3	23,0	8,37	2,12
196	P52926	High mobility group protein HMGI-C	HMGA2	11,8	10,62	0,48
197	P16403	Histone H1.2	HIST1H1C	21,4	10,93	0,59
198	P16402	Histone H1.3	HIST1H1D	22,3	11,02	0,59
199	P10412	Histone H1.4	HIST1H1E	21,9	11,03	0,59
200	P16401	Histone H1.5	HIST1H1B	22,6	10,92	0,40
201	Q92522	Histone H1x	H1FX	22,5	10,76	hoch
202	Q71UI9	Histone H2A.V	H2AFV	13,5	10,58	0,58
203	P0C0S5	Histone H2A.Z	H2AFZ	13,5	10,58	0,58
204	P62805	Histone H4	HIST1H4A	11,4	11,36	0,53
205	Q86X55	Histone-arginine methyltransferase CARM1	CARM1	65,8	6,73	runter
206	Q09028	Histone-binding protein RBBP4	RBBP4	47,6	4,89	3,01
207	P05534	HLA class I histocompatibility antigen, A-24 alpha chain	HLA-A	40,7	6,34	1,76
208	P30685	HLA class I histocompatibility antigen, B-35 alpha chain	HLA-B	40,4	6,46	1,60
209	P30483	HLA class I histocompatibility antigen, B-45 alpha chain	HLA-B	40,4	6,47	1,60
210	P30487	HLA class I histocompatibility antigen, B-49 alpha chain	HLA-B	40,6	6,47	1,60
211	P30488	HLA class I histocompatibility antigen, B-50 alpha chain	HLA-B	40,5	6,47	1,60
212	P30491	HLA class I histocompatibility antigen, B-53 alpha chain	HLA-B	40,5	6,46	1,60
213	P10319	HLA class I histocompatibility antigen, B-58 alpha chain	HLA-B	40,3	6,30	1,60
214	P30508	HLA class I histocompatibility antigen, Cw-12 alpha chain	HLA-C	40,9	6,30	1,60
215	Q07000	HLA class I histocompatibility antigen, Cw-15 alpha chain	HLA-C	40,8	6,33	1,60
216	Q95604	HLA class I histocompatibility antigen, Cw-17 alpha chain	HLA-C	41,2	6,80	1,60
217	P30501	HLA class I histocompatibility antigen, Cw-2 alpha chain	HLA-C	41,1	6,11	1,60
218	P30504	HLA class I histocompatibility antigen, Cw-4 alpha chain	HLA-C	41,0	6,47	hoch
219	Q9TNN7	HLA class I histocompatibility antigen, Cw-5 alpha chain	HLA-C	40,9	7,44	1,60

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs*. siNNMT
220	P30505	HLA class I histocompatibility antigen, Cw-8 alpha chain	HLA-C	40,7	6,98	1,60
221	Q16543	Hsp90 co-chaperone Cdc37	CDC37	44,4	5,25	0,55
222	O00629	Importin subunit alpha-3	KPNA4	57,9	4,96	0,40
223	O60684	Importin subunit alpha-7	KPNA6	60,0	4,98	1,79
224	Q14974	Importin subunit beta-1	KPNB1	97,1	4,78	0,63
225	O95373	Importin-7	IPO7	119,4	4,82	0,28
226	Q70UQ0	Inhibitor of nuclear factor kappa-B kinase-interacting protein	IKBIP	39,3	9,17	2,02
227	Q16270	Insulin-like growth factor-binding protein 7	IGFBP7	29,1	7,90	1,60
228	P26006	Integrin alpha-3	ITGA3	116,5	6,77	0,64
229	P18084	Integrin beta-5	ITGB5	88,0	6,06	runter
230	Q13418	Integrin-linked protein kinase	ILK	51,4	8,07	1,50
231	P19525	Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	62,1	8,40	1,85
232	Q12905	Interleukin enhancer-binding factor 2	ILF2	43,0	5,26	0,47
233	Q14116	Interleukin-18	IL18	22,3	4,67	1,55
234	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic	IDH1	46,6	7,01	0,41
235	Q13907	Isopentenyl-diphosphate Delta-isomerase 1	IDI1	26,3	6,34	1,70
236	P14923	Junction plakoglobin	JUP	81,7	6,14	0,66
237	Q04760	Lactoylglutathione lyase	GLO1	20,8	5,31	1,91
238	Q14739	Lamin-B receptor	LBR	70,7	9,36	runter
239	P07942	Laminin subunit beta-1	LAMB1	197,9	4,94	0,61
240	Q6PKG0	La-related protein 1	LARP1	123,4	8,82	3,87
241	Q01650	Large neutral amino acids transporter small subunit 1	SLC7A5	55,0	7,72	0,60
242	Q8NC56	LEM domain-containing protein 2	LEMD2	56,9	9,00	0,63
243	Q9P2J5	Leucine--tRNA ligase, cytoplasmic	LARS	134,4	7,30	0,60
244	P48059	LIM and senescent cell antigen-like-containing domain protein 1	LIMS1	37,2	8,05	0,44
245	Q9UHB6	LIM domain and actin-binding protein 1	LIMA1	85,2	6,84	2,78
246	P36776	Lon protease homolog, mitochondrial	LONP1	106,4	6,39	0,59
247	P33121	Long-chain-fatty-acid--CoA ligase 1	ACSL1	77,9	7,15	0,57
248	O60488	Long-chain-fatty-acid--CoA ligase 4	ACSL4	79,1	8,38	1,85
249	P42785	Lysosomal Pro-X carboxypeptidase	PRCP	55,8	7,21	1,90
250	Q9Y4K0	Lysyl oxidase homolog 2	LOXL2	86,7	6,38	0,50
251	P40121	Macrophage-capping protein	CAPG	38,5	6,19	1,60
252	Q9UNF1	Melanoma-associated antigen D2	MAGED2	64,9	9,32	1,51
253	O94776	Metastasis-associated protein MTA2	MTA2	75,0	9,66	0,58
254	P56192	Methionine--tRNA ligase, cytoplasmic	MARS	101,1	6,16	1,50
255	Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	MCCC2	61,3	7,68	1,82

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256	Q96GX9	Methylthioribulose-1-phosphate dehydratase	APIP	27,1	7,12	1,91
257	Q7Z434	Mitochondrial antiviral-signaling protein	MAVS	56,5	5,52	0,47
258	O43615	Mitochondrial import inner membrane translocase subunit TIM44	TIMM44	51,3	8,32	0,62
259	Q15785	Mitochondrial import receptor subunit TOM34	TOMM34	34,5	8,98	1,50
260	O75439	Mitochondrial-processing peptidase subunit beta	PMPCB	54,3	6,83	1,54
261	P28482	Mitogen-activated protein kinase 1	MAPK1	41,4	6,98	runter
262	Q16539	Mitogen-activated protein kinase 14	MAPK14	41,3	5,78	2,10
263	Q9BYG3	MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK	34,2	9,88	0,60
264	Q96T76	MMS19 nucleotide excision repair protein homolog	MMS19	113,2	6,35	1,69
265	P26038	Moesin	MSN	67,8	6,40	1,57
266	P53985	Monocarboxylate transporter 1	SLC16A1	53,9	8,66	runter
267	O43148	mRNA cap guanine-N7 methyltransferase	RNMT	54,8	6,61	0,64
268	Q9BQG0	Myb-binding protein 1A	MYBBP1A	148,8	9,28	0,54
269	P35580	Myosin-10	MYH10	228,9	5,54	0,49
270	O95865	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	DDAH2	29,6	6,01	0,56
271	O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	SLC9A3R1	38,8	5,77	1,53
272	Q86SF2	N-acetylgalactosaminyltransferase 7	GALNT7	75,3	7,11	0,36
273	P15586	N-acetylglucosamine-6-sulfatase	GNS	62,0	8,31	1,63
274	P23368	NAD-dependent malic enzyme, mitochondrial	ME2	65,4	7,61	1,80
275	Q9NXA8	NAD-dependent protein deacylase sirtuin-5, mitochondrial	SIRT5	33,9	8,47	0,55
276	O96000	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NDUFB10	20,8	8,48	4,07
277	P00387	NADH-cytochrome b5 reductase 3	CYB5R3	34,2	7,59	0,61
278	P48163	NADP-dependent malic enzyme	ME1	64,1	6,13	2,27
279	P41227	N-alpha-acetyltransferase 10	NAA10	26,4	5,64	hoch
280	Q8WX92	Negative elongation factor B	NELFB	65,7	6,13	runter
281	Q9UMX5	Neudesin	NENF	18,8	5,69	hoch
282	Q15758	Neutral amino acid transporter B(0)	SLC1A5	56,6	5,48	0,51
283	**P40261**	**Nicotinamide N-methyltransferase**	**NNMT**	**29,6**	**5,74**	**0,07**
284	P22307	Non-specific lipid-transfer protein	SCP2	59,0	6,89	hoch
285	Q9UNZ2	NSFL1 cofactor p47	NSFL1C	40,5	5,10	1,53
286	P49321	Nuclear autoantigenic sperm protein	NASP	85,2	4,30	0,40
287	Q00653	Nuclear factor NF-kappa-B p100 subunit	NFKB2	96,7	6,25	1,71
288	Q12972	Nuclear inhibitor of protein phosphatase 1	PPP1R8	38,5	7,37	hoch
289	Q9Y266	Nuclear migration protein nudC	NUDC	38,2	5,38	1,85
290	Q92621	Nuclear pore complex protein Nup205	NUP205	227,8	6,19	runter
291	Q8N1F7	Nuclear pore complex protein Nup93	NUP93	93,4	5,72	0,48

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292	P52948	Nuclear pore complex protein Nup98-Nup96	NUP98	197,5	6,40	runter
293	P37198	Nuclear pore glycoprotein p62	NUP62	53,2	5,31	1,92
294	Q8TEM1	Nuclear pore membrane glycoprotein 210	NUP210	205,0	6,81	runter
295	P80303	Nucleobindin-2	NUCB2	50,2	5,12	1,72
296	O00567	Nucleolar protein 56	NOP56	66,0	9,19	0,45
297	Q9Y2X3	Nucleolar protein 58	NOP58	59,5	8,92	0,45
298	P17480	Nucleolar transcription factor 1	UBTF	89,4	5,81	runter
299	Q01085	Nucleolysin TIAR	TIAL1	41,6	7,74	0,65
300	P12270	Nucleoprotein TPR	TPR	267,1	5,02	0,59
301	P15531	Nucleoside diphosphate kinase A	NME1	17,1	6,19	1,69
302	P22392	Nucleoside diphosphate kinase B	NME2	17,3	8,41	2,35
303	Q9NX40	OCIA domain-containing protein 1	OCIAD1	27,6	7,49	hoch
304	Q9NQR4	Omega-amidase NIT2	NIT2	30,6	7,21	1,98
305	Q9NZT2	Opioid growth factor receptor	OGFR	73,3	4,84	0,63
306	P36551	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	CPOX	50,1	8,25	1,81
307	Q9BZF1	Oxysterol-binding protein-related protein 8	OSBPL8	101,1	6,96	runter
308	Q06710	Paired box protein Pax-8	PAX8	48,2	7,84	hoch
309	Q9BRP8	Partner of Y14 and mago	PYM1	22,6	9,45	1,53
310	P26885	Peptidyl-prolyl cis-trans isomerase FKBP2	FKBP2	15,6	9,13	0,53
311	Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3	FKBP3	25,2	9,28	1,73
312	Q14318	Peptidyl-prolyl cis-trans isomerase FKBP8	FKBP8	44,5	4,84	1,56
313	Q13526	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	PIN1	18,2	8,82	1,54
314	Q9Y237	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	PIN4	13,8	9,77	1,64
315	Q06830	Peroxiredoxin-1	PRDX1	22,1	8,13	1,72
316	P30044	Peroxiredoxin-5, mitochondrial	PRDX5	22,1	8,70	0,45
317	O00541	Pescadillo homolog	S1	68,0	7,33	1,57
318	Q00325	Phosphate carrier protein, mitochondrial	SLC25A3	40,1	9,38	0,65
319	P48739	Phosphatidylinositol transfer protein beta isoform	PITPNB	31,5	6,87	hoch
320	Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	70,7	7,62	0,20
321	P15259	Phosphoglycerate mutase 2	PGAM2	28,7	8,88	1,61
322	Q14558	Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	39,4	7,20	1,65
323	Q9Y617	Phosphoserine aminotransferase	PSAT1	40,4	7,66	0,66
324	P05121	Plasminogen activator inhibitor 1	SERPINE1	45,0	7,20	hoch
325	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein	SERBP1	44,9	8,65	1,58
326	Q14651	Plastin-1	PLS1	70,2	5,41	0,55
327	P13797	Plastin-3	PLS3	70,8	5,60	1,51
328	Q15149	Plectin	PLEC	531,5	5,96	0,40

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329	P09874	Poly [ADP-ribose] polymerase 1	PARP1	113,0	8,88	0,58
330	Q6NZI2	Polymerase I and transcript release factor	PTRF	43,5	5,60	1,51
331	Q10471	Polypeptide N-acetylgalactosaminyltransferase 2	GALNT2	64,7	8,35	1,87
332	P61758	Prefoldin subunit 3	VBP1	22,6	7,11	2,36
333	Q15007	Pre-mRNA-splicing regulator WTAP	WTAP	44,2	5,19	1,63
334	Q7L014	Probable ATP-dependent RNA helicase DDX46	DDX46	117,3	9,29	0,65
335	Q53EL6	Programmed cell death protein 4	PDCD4	51,7	5,21	1,74
336	P35232	Prohibitin	PHB	29,8	5,76	0,41
337	Q99623	Prohibitin-2	PHB2	33,3	9,83	0,55
338	Q9UQ80	Proliferation-associated protein 2G4	PA2G4	43,8	6,55	1,62
339	Q32P28	Prolyl 3-hydroxylase 1	P3H1	83,3	5,14	1,55
340	P13674	Prolyl 4-hydroxylase subunit alpha-1	P4HA1	61,0	6,01	1,50
341	P25786	Proteasome subunit alpha type-1	PSMA1	29,5	6,61	1,74
342	P25788	Proteasome subunit alpha type-3	PSMA3	28,4	5,33	1,54
343	Q99436	Proteasome subunit beta type-7	PSMB7	29,9	7,68	1,79
344	P28062	Proteasome subunit beta type-8	PSMB8	30,3	7,43	1,76
345	Q8IVF2	Protein AHNAK2	AHNAK2	616,2	5,36	1,78
346	Q9BT09	Protein canopy homolog 3	CNPY3	30,7	5,49	hoch
347	P30101	Protein disulfide-isomerase A3	PDIA3	56,7	6,35	1,61
348	P13667	Protein disulfide-isomerase A4	PDIA4	72,9	5,07	1,63
349	Q14554	Protein disulfide-isomerase A5	PDIA5	59,6	7,91	2,04
350	Q92520	Protein FAM3C	FAM3C	24,7	8,29	2,57
351	Q13045	Protein flightless-1 homolog	FLII	144,7	6,05	runter
352	P17252	Protein kinase C alpha type	PRKCA	76,7	7,05	0,65
353	P05771	Protein kinase C beta type	PRKCB	76,8	7,01	0,66
354	Q86UE4	Protein LYRIC	MTDH	63,8	9,32	0,63
355	Q9BZQ8	Protein Niban	FAM129A	103,1	4,78	0,49
356	O75323	Protein NipSnap homolog 2	GBAS	33,7	9,36	hoch
357	Q96C90	Protein phosphatase 1 regulatory subunit 14B	PPP1R14B	15,9	4,86	0,47
358	Q15435	Protein phosphatase 1 regulatory subunit 7	PPP1R7	41,5	4,91	1,53
359	P41236	Protein phosphatase inhibitor 2	PPP1R2	23,0	4,74	1,56
360	Q6NXS1	Protein phosphatase inhibitor 2-like protein 3	PPP1R2P3	23,0	4,92	1,56
361	P31949	Protein S100-A11	S100A11	11,7	7,12	0,40
362	Q96FQ6	Protein S100-A16	S100A16	11,8	6,79	1,68
363	Q01105	Protein SET	SET	33,5	4,32	0,63
364	P0DME0	Protein SETSIP	SETSIP	34,9	4,31	0,59
365	Q969Z0	Protein TBRG4	TBRG4	70,7	7,42	runter

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366	P21980	Protein-glutamine gamma-glutamyltransferase 2	TGM2	77,3	5,22	0,42
367	P12931	Proto-oncogene tyrosine-protein kinase Src	SRC	59,8	7,42	runter
368	P61457	Pterin-4-alpha-carbinolamine dehydratase	PCBD1	12,0	6,80	0,37
369	P55786	Puromycin-sensitive aminopeptidase	NPPS	103,2	5,72	0,61
370	Q5VTE0	Putative elongation factor 1-alpha-like 3	EEF1A1P5	50,2	9,07	1,51
371	Q58FG0	Putative heat shock protein HSP 90-alpha A5	HSP90AA5P	38,7	6,57	0,42
372	Q2TB90	Putative hexokinase HKDC1	HKDC1	102,5	7,12	1,67
373	B2RPK0	Putative high mobility group protein B1-like 1	HMGB1P1	24,2	6,21	2,33
374	O60361	Putative nucleoside diphosphate kinase	NME2P1	15,5	8,57	2,56
375	Q49A26	Putative oxidoreductase GLYR1	GLYR1	60,5	9,17	runter
376	Q9NVS9	Pyridoxine-5'-phosphate oxidase	PNPO	30,0	7,06	runter
377	P32322	Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1	33,3	7,61	0,50
378	O00330	Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	54,1	8,66	0,16
379	P35241	Radixin	RDX	68,5	6,37	1,72
380	Q5VZM2	Ras-related GTP-binding protein B	RRAGB	43,2	6,21	3,21
381	P61106	Ras-related protein Rab-14	RAB14	23,9	6,21	runter
382	Q9H0U4	Ras-related protein Rab-1B	RAB1B	22,2	5,73	runter
383	P61019	Ras-related protein Rab-2A	RAB2A	23,5	6,54	0,36
384	Q8WUD1	Ras-related protein Rab-2B	RAB2B	24,2	7,83	0,22
385	P51148	Ras-related protein Rab-5C	RAB5C	23,5	8,41	0,53
386	P51149	Ras-related protein Rab-7a	RAB7A	23,5	6,70	0,56
387	P11233	Ras-related protein Ral-A	RALA	23,6	7,11	runter
388	P10301	Ras-related protein R-Ras	RRAS	23,5	6,93	0,33
389	P18754	Regulator of chromosome condensation	RCC1	44,9	7,52	0,49
390	P35250	Replication factor C subunit 2	RFC2	39,1	6,44	0,65
391	P15927	Replication protein A 32 kDa subunit	RPA2	29,2	6,15	1,94
392	Q9NQC3	Reticulon-4	RTN4	129,9	4,50	0,52
393	P00352	Retinal dehydrogenase 1	ALDH1A1	54,8	6,73	0,63
394	P84095	Rho-related GTP-binding protein RhoG	RHOG	21,3	8,12	runter
395	P21108	Ribose-phosphate pyrophosphokinase 3	PRPS1L1	34,8	6,35	0,32
396	O76021	Ribosomal L1 domain-containing protein 1	RSL1D1	54,9	10,13	0,50
397	Q9Y3A5	Ribosome maturation protein SBDS	SBDS	28,7	8,75	2,14
398	Q9H0A0	RNA cytidine acetyltransferase	NAT10	115,7	8,27	0,62
399	Q96PK6	RNA-binding protein 14	RBM14	69,4	9,67	0,58
400	O14983	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	ATP2A1	110,2	5,16	0,42
401	P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	114,7	5,34	0,52
402	Q08AF3	Schlafen family member 5	SLFN5	101,0	8,22	runter

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403	Q8WVM8	Sec1 family domain-containing protein 1	SCFD1	72,3	6,27	runter
404	Q92599	Septin-8	39692	55,7	6,28	2,71
405	O15269	Serine palmitoyltransferase 1	SPTLC1	52,7	6,01	runter
406	Q92743	Serine protease HTRA1	HTRA1	51,3	7,83	1,77
407	Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	299,4	12,06	0,56
408	Q16629	Serine/arginine-rich splicing factor 7	SRSF7	27,4	11,82	6,09
409	Q9Y6E0	Serine/threonine-protein kinase 24	STK24	49,3	5,69	0,55
410	Q9P289	Serine/threonine-protein kinase 26	STK26	46,5	5,29	0,30
411	Q13177	Serine/threonine-protein kinase PAK 2	PAK2	58,0	5,96	1,70
412	P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	65,3	5,11	1,66
413	O00743	Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C	35,1	5,69	runter
414	Q5H9R7	Serine/threonine-protein phosphatase 6 regulatory subunit 3	PPP6R3	97,6	4,60	0,35
415	Q9BRF8	Serine/threonine-protein phosphatase CPPED1	CPD1	35,5	6,20	runter
416	Q96B97	SH3 domain-containing kinase-binding protein 1	SH3KBP1	73,1	6,62	hoch
417	P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB	47,5	6,99	1,62
418	Q15005	Signal peptidase complex subunit 2	SPCS2	25,0	8,47	1,59
419	P42224	Signal transducer and activator of transcription 1-alpha/beta	STAT1	87,3	6,05	1,69
420	Q92783	Signal transducing adapter molecule 1	STAM	59,1	4,82	2,23
421	P63162	Small nuclear ribonucleoprotein-associated protein N	SNRPN	24,6	11,19	0,45
422	P14678	Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	24,6	11,19	0,45
423	P05026	Sodium/potassium-transporting ATPase subunit beta-1	ATP1B1	35,0	8,53	hoch
424	Q01082	Spectrin beta chain, non-erythrocytic 1	SPTBN1	274,4	5,57	0,48
425	P63208	S-phase kinase-associated protein 1	SKP1	18,6	4,54	2,10
426	O75533	Splicing factor 3B subunit 1	SF3B1	145,7	7,09	0,65
427	Q96I25	Splicing factor 45	RBM17	44,9	5,97	hoch
428	Q15020	Squamous cell carcinoma antigen recognized by T-cells 3	SART3	109,9	5,57	0,62
429	O95630	STAM-binding protein	STAMBP	48,0	6,29	hoch
430	Q15738	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	NSDHL	41,9	8,06	0,49
431	Q96I99	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	46,5	6,39	0,64
432	O94901	SUN domain-containing protein 1	SUN1	90,0	7,08	runter
433	P04179	Superoxide dismutase [Mn], mitochondrial	SOD2	24,7	8,25	1,71
434	Q8TAQ2	SWI/SNF complex subunit SMARCC2	SMARCC2	132,8	5,69	hoch
435	O60264	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	121,8	8,09	0,58
436	Q969G3	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	SMARCE1	46,6	4,88	0,30

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs*. siNNMT
437	O15400	Syntaxin-7	STX7	29,8	5,55	1,64
438	P24821	Tenascin	TNC	240,7	4,89	runter
439	Q68CZ2	Tensin-3	TNS3	155,2	6,81	runter
440	P52888	Thimet oligopeptidase	THOP1	78,8	6,05	hoch
441	O95881	Thioredoxin domain-containing protein 12	TXNDC12	19,2	5,40	1,62
442	Q9H3N1	Thioredoxin-related transmembrane protein 1	TMX1	31,8	4,98	0,51
443	Q9NXG2	THUMP domain-containing protein 1	THUMPD1	39,3	7,88	runter
444	P62328	Thymosin beta-4	TMSB4X	5,1	5,06	2,01
445	Q9Y2W1	Thyroid hormone receptor-associated protein 3	THRAP3	108,6	10,15	0,65
446	O75663	TIP41-like protein	TIPRL	31,4	5,91	1,91
447	Q04206	Transcription factor p65	RELA	60,2	5,68	0,36
448	P02786	Transferrin receptor protein 1	TFRC	84,8	6,61	0,65
449	Q13595	Transformer-2 protein homolog alpha	TRA2A	32,7	11,27	hoch
450	P37802	Transgelin-2	TAGLN2	22,4	8,25	1,63
451	Q9UI10	Translation initiation factor eIF-2B subunit delta	EIF2B4	57,5	9,38	hoch
452	P13693	Translationally-controlled tumor protein	TPT1	19,6	4,93	1,65
453	Q15631	Translin	TSN	26,2	6,44	runter
454	Q99598	Translin-associated protein X	TSNAX	33,1	6,55	3,87
455	Q15629	Translocating chain-associated membrane protein 1	TRAM1	43,0	9,63	0,65
456	Q9HD45	Transmembrane 9 superfamily member 3	TM9SF3	67,8	7,21	0,57
457	Q92544	Transmembrane 9 superfamily member 4	TM9SF4	74,5	6,54	0,66
458	Q9Y3B3	Transmembrane emp24 domain-containing protein 7	TMED7	25,2	6,89	0,50
459	Q9BTV4	Transmembrane protein 43	TMEM43	44,8	8,13	0,29
460	Q92973	Transportin-1	TNPO1	102,3	4,98	0,64
461	Q9Y5L0	Transportin-3	TNPO3	104,1	5,57	runter
462	P53007	Tricarboxylate transport protein, mitochondrial	SLC25A1	34,0	9,89	0,47
463	P22102	Trifunctional purine biosynthetic protein adenosine-3	GART	107,7	6,70	0,48
464	Q7Z2T5	TRMT1-like protein	TRMT1L	81,7	7,88	1,89
465	P09493	Tropomyosin alpha-1 chain	TPM1	32,7	4,74	1,61
466	P07951	Tropomyosin beta chain	TPM2	32,8	4,70	2,86
467	P04350	Tubulin beta-4A chain	TUBB4A	49,6	4,88	0,33
468	P68371	Tubulin beta-4B chain	TUBB4B	49,8	4,89	hoch
469	O75347	Tubulin-specific chaperone A	TBCA	12,8	5,29	1,79
470	Q9BTW9	Tubulin-specific chaperone D	TBCD	132,5	6,19	0,47
471	Q14166	Tubulin--tyrosine ligase-like protein 12	TTLL12	74,4	5,53	1,52
472	Q9Y2Z4	Tyrosine--tRNA ligase, mitochondrial	YARS2	53,2	8,98	runter

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs*. siNNMT
473	Q8WWY3	U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	55,4	5,78	0,66
474	Q53GS9	U4/U6.U5 tri-snRNP-associated protein 2	USP39	65,3	8,91	0,66
475	Q9UMX0	Ubiquilin-1	UBQLN1	62,5	5,11	1,81
476	Q9NRR5	Ubiquilin-4	UBQLN4	63,8	5,22	0,66
477	Q96FW1	Ubiquitin thioesterase OTUB1	OTUB1	31,3	4,94	0,65
478	Q13404	Ubiquitin-conjugating enzyme E2 variant 1	UBE2V1	16,5	7,93	1,61
479	Q15819	Ubiquitin-conjugating enzyme E2 variant 2	UBE2V2	16,4	8,09	2,00
480	Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1	UGGT1	177,1	5,63	0,66
481	O43795	Unconventional myosin-Ib	MYO1B	131,9	9,38	1,53
482	O00159	Unconventional myosin-Ic	MYO1C	121,6	9,41	0,62
483	Q16851	UTP--glucose-1-phosphate uridylyltransferase	UGP2	56,9	8,15	1,56
484	P46939	Utrophin	UTRN	394,2	5,33	hoch
485	P54727	UV excision repair protein RAD23 homolog B	RAD23B	43,1	4,84	1,56
486	Q96QK1	Vacuolar protein sorting-associated protein 35	VPS35	91,6	5,49	0,62
487	P19320	Vascular cell adhesion protein 1	VCAM1	81,2	5,22	2,18
488	P50552	Vasodilator-stimulated phosphoprotein	VASP	39,8	8,94	2,74
489	Q53GQ0	Very-long-chain 3-oxoacyl-CoA reductase	HSD17B12	34,3	9,32	0,47
490	P08670	Vimentin	VIM	53,6	5,12	1,76
491	Q8IWB7	WD repeat and FYVE domain-containing protein 1	WDFY1	46,3	7,33	0,60
492	P61964	WD repeat-containing protein 5	WDR5	36,6	8,27	hoch
493	Q9GZS3	WD repeat-containing protein 61	WDR61	33,6	5,47	1,78
494	P13010	X-ray repair cross-complementing protein 5	XRCC5	82,7	5,81	0,55
495	Q96ME7	Zinc finger protein 512	ZNF512	64,6	9,76	runter

Tabelle S5: Differenziell exprimierte Proteine von transient transfizierten Caki-2 Zellen bei 100 µM Methionin (mock *vs*. NNMT)

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs.* NNMT
1	P09543	2',3'-cyclic-nucleotide 3'-phosphodiesterase	CNP	47,5	9,07	0,66
2	P51665	26S proteasome non-ATPase regulatory subunit 7	PSMD7	37,0	6,77	2,88
3	Q9Y2R9	28S ribosomal protein S7, mitochondrial	MRPS7	28,1	9,99	hoch
4	Q9BRJ2	39S ribosomal protein L45, mitochondrial	MRPL45	35,3	9,03	1,68
5	P42765	3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	41,9	8,09	1,65
6	P25325	3-mercaptopyruvate sulfurtransferase	MPST	33,2	6,60	1,52
7	P62277	40S ribosomal protein S13	RPS13	17,2	10,54	2,68
8	P08708	40S ribosomal protein S17	RPS17	15,5	9,85	0,60

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs.* NNMT
9	P62847	40S ribosomal protein S24	RPS24	15,4	10,78	1,51
10	P62753	40S ribosomal protein S6	RPS6	28,7	10,84	1,66
11	Q13131	5'-AMP-activated protein kinase catalytic subunit alpha-1	PRKAA1	64,0	8,12	0,52
12	Q5TFE4	5'-nucleotidase domain-containing protein 1	NT5DC1	51,8	6,35	0,60
13	P62750	60S ribosomal protein L23a	RPL23A	17,7	10,45	0,62
14	P61254	60S ribosomal protein L26	RPL26	17,2	10,55	1,55
15	Q9UNX3	60S ribosomal protein L26-like 1	RPL26L1	17,2	10,55	1,60
16	P46779	60S ribosomal protein L28	RPL28	15,7	12,02	0,60
17	O15145	Actin-related protein 2/3 complex subunit 3	ARPC3	20,5	8,59	0,49
18	Q9H845	Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	68,7	7,96	runter
19	P07108	Acyl-CoA-binding protein	DBI	10,0	6,57	0,59
20	P23526	Adenosylhomocysteinase	AHCY	47,7	6,34	0,66
21	P54819	Adenylate kinase 2, mitochondrial	AK2	26,5	7,81	1,63
22	P84077	ADP-ribosylation factor 1	ARF1	20,7	6,80	0,64
23	P61204	ADP-ribosylation factor 3	ARF3	20,6	7,43	0,64
24	P62330	ADP-ribosylation factor 6	ARF6	20,1	8,95	0,49
25	P14550	Alcohol dehydrogenase [NADP(+)]	AKR1A1	36,6	6,79	0,44
26	P52895	Aldo-keto reductase family 1 member C2	AKR1C2	36,7	7,49	0,53
27	P30533	Alpha-2-macroglobulin receptor-associated protein	LRPAP1	41,4	8,78	runter
28	Q03518	Antigen peptide transporter 1	TAP1	87,2	8,02	2,12
29	O14617	AP-3 complex subunit delta-1	AP3D1	130,1	8,48	2,16
30	Q15121	Astrocytic phosphoprotein PEA-15	A15	15,0	5,02	0,57
31	Q8WWM7	Ataxin-2-like protein	ATXN2L	113,3	8,59	2,20
32	Q9NVI7	ATPase family AAA domain-containing protein 3A	ATAD3A	71,3	8,98	2,55
33	Q5T2N8	ATPase family AAA domain-containing protein 3C	ATAD3C	46,4	9,31	1,61
34	O75531	Barrier-to-autointegration factor	BANF1	10,1	6,09	0,58
35	Q9Y6E2	Basic leucine zipper and W2 domain-containing protein 2	BZW2	48,1	6,68	0,58
36	Q562R1	Beta-actin-like protein 2	ACTBL2	42,0	5,59	26,52
37	P42025	Beta-centractin	ACTR1B	42,3	6,40	runter
38	Q9P287	BRCA2 and CDKN1A-interacting protein	BCCIP	36,0	4,61	0,50
39	Q13895	Bystin	BYSL	49,6	8,12	runter
40	Q6NUK1	Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	53,3	6,33	2,61
41	Q05682	Caldesmon	CALD1	93,2	5,66	0,47
42	O75828	Carbonyl reductase [NADPH] 3	CBR3	30,8	6,18	0,49
43	Q96DG6	Carboxymethylenebutenolidase homolog	CMBL	28,0	7,18	0,64
44	P04040	Catalase	CAT	59,7	7,39	0,52
45	P35221	Catenin alpha-1	CTNNA1	100,0	6,29	0,63

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs.* NNMT
46	Q96JB5	CDK5 regulatory subunit-associated protein 3	CDK5RAP3	56,9	4,75	0,52
47	Q9NZZ3	Charged multivesicular body protein 5	CHMP5	24,6	4,83	1,87
48	P49585	Choline-phosphate cytidylyltransferase A	PCYT1A	41,7	7,25	runter
49	Q14839	Chromodomain-helicase-DNA-binding protein 4	CHD4	217,9	5,86	1,72
50	P09496	Clathrin light chain A	CLTA	27,1	4,51	0,53
51	Q9UBF2	Coatomer subunit gamma-2	COPG2	97,6	5,81	0,27
52	Q96CT7	Coiled-coil domain-containing protein 124	CCDC124	25,8	9,54	runter
53	Q14011	Cold-inducible RNA-binding protein	CIRBP	18,6	9,51	0,61
54	Q9BT78	COP9 signalosome complex subunit 4	COPS4	46,2	5,83	2,42
55	Q9UBG0	C-type mannose receptor 2	MRC2	166,6	5,83	0,53
56	Q13617	Cullin-2	CUL2	86,9	6,92	2,12
57	P22695	Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	48,4	8,63	0,58
58	Q9HCS2	Cytochrome P450 4F12	CYP4F12	60,2	7,39	4,53
59	Q7L576	Cytoplasmic FMR1-interacting protein 1	CYFIP1	145,1	6,90	1,52
60	P49366	Deoxyhypusine synthase	DHPS	40,9	5,36	1,77
61	P11388	DNA topoisomerase 2-alpha	TOP2A	174,3	8,72	2,10
62	Q96EY1	DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	52,5	9,26	2,39
63	Q99543	DnaJ homolog subfamily C member 2	DNAJC2	72,0	8,70	0,43
64	Q13217	DnaJ homolog subfamily C member 3	DNAJC3	57,5	6,15	0,48
65	O75937	DnaJ homolog subfamily C member 8	DNAJC8	29,8	9,06	1,94
66	Q08477	Docosahexaenoic acid omega-hydroxylase CYP4F3	CYP4F3	59,8	7,64	3,09
67	Q9NUL3	Double-stranded RNA-binding protein Staufen homolog 2	STAU2	62,6	9,61	hoch
68	Q02750	Dual specificity mitogen-activated protein kinase kinase 1	MAP2K1	43,4	6,62	runter
69	P36507	Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	44,4	6,55	3,46
70	Q14203	Dynactin subunit 1	DCTN1	141,6	5,81	2,33
71	Q9UJW0	Dynactin subunit 4	DCTN4	52,3	7,34	runter
72	O60313	Dynamin-like 120 kDa protein, mitochondrial	OPA1	111,6	7,87	2,83
73	Q9UII4	E3 ISG15--protein ligase HERC5	HERC5	116,8	7,65	1,54
74	Q14258	E3 ubiquitin/ISG15 ligase TRIM25	TRIM25	70,9	8,09	1,90
75	Q9P0J7	E3 ubiquitin-protein ligase KCMF1	KCMF1	41,9	5,66	0,30
76	Q96C19	EF-hand domain-containing protein D2	EFHD2	26,7	5,20	0,62
77	Q92616	eIF-2-alpha kinase activator GCN1	GCN1	292,6	7,47	1,61
78	Q8N766	ER membrane protein complex subunit 1	EMC1	111,7	7,66	runter
79	P38919	Eukaryotic initiation factor 4A-III	EIF4A3	46,8	6,73	0,56
80	O15372	Eukaryotic translation initiation factor 3 subunit H	EIF3H	39,9	6,54	1,76
81	P23588	Eukaryotic translation initiation factor 4B	EIF4B	69,1	5,73	0,64
82	P06730	Eukaryotic translation initiation factor 4E	EIF4E	25,1	6,15	3,34

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs.* NNMT
83	Q15056	Eukaryotic translation initiation factor 4H	EIF4H	27,4	7,23	0,47
84	P49327	Fatty acid synthase	FASN	273,3	6,44	1,66
85	P51648	Fatty aldehyde dehydrogenase	ALDH3A2	54,8	7,88	0,62
86	O60907	F-box-like/WD repeat-containing protein TBL1X	TBL1X	62,5	6,55	1,66
87	P04062	Glucosylceramidase	GBA	59,7	7,61	1,74
88	O00461	Golgi integral membrane protein 4	GOLIM4	81,8	4,77	0,39
89	Q08378	Golgin subfamily A member 3	GOLGA3	167,3	5,44	1,50
90	Q9Y450	HBS1-like protein	HBS1L	75,4	6,61	1,60
91	Q14568	Heat shock protein HSP 90-alpha A2	HSP90AA2P	39,3	4,65	1,86
92	P17096	High mobility group protein HMG-I/HMG-Y	HMGA1	11,7	10,32	0,64
93	P52926	High mobility group protein HMGI-C	HMGA2	11,8	10,62	0,30
94	P16401	Histone H1.5	HIST1H1B	22,6	10,92	1,68
95	P04908	Histone H2A type 1-B/E	HIST1H2AB	14,1	11,05	1,65
96	Q93077	Histone H2A type 1-C	HIST1H2AC	14,1	11,05	1,65
97	Q7L7L0	Histone H2A type 3	HIST3H2A	14,1	11,05	1,65
98	P68431	Histone H3.1	HIST1H3A	15,4	11,12	1,84
99	Q71DI3	Histone H3.2	HIST2H3A	15,4	11,27	1,95
100	Q86X55	Histone-arginine methyltransferase CARM1	CARM1	65,8	6,73	runter
101	Q16576	Histone-binding protein RBBP7	RBBP7	47,8	5,05	2,05
102	Q16543	Hsp90 co-chaperone Cdc37	CDC37	44,4	5,25	0,44
103	Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HADH	34,3	8,85	1,69
104	O00629	Importin subunit alpha-3	KPNA4	57,9	4,96	2,82
105	Q70UQ0	Inhibitor of nuclear factor kappa-B kinase-interacting protein	IKBIP	39,3	9,17	4,97
106	Q15181	Inorganic pyrophosphatase	PPA1	32,6	5,86	0,66
107	P80217	Interferon-induced 35 kDa protein	IFI35	31,5	6,09	0,60
108	O75569	Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	34,4	8,41	0,54
109	Q14116	Interleukin-18	IL18	22,3	4,67	hoch
110	Q9H0B6	Kinesin light chain 2	KLC2	68,9	7,15	hoch
111	P11047	Laminin subunit gamma-1	LAMC1	177,5	5,12	0,39
112	Q6PKG0	La-related protein 1	LARP1	123,4	8,82	3,49
113	P46379	Large proline-rich protein BAG6	BAG6	119,3	5,60	1,94
114	P09960	Leukotriene A-4 hydrolase	LTA4H	69,2	6,18	0,44
115	Q9UHB6	LIM domain and actin-binding protein 1	LIMA1	85,2	6,84	0,61
116	P33121	Long-chain-fatty-acid--CoA ligase 1	ACSL1	77,9	7,15	runter
117	P49006	MARCKS-related protein	MARCKSL1	19,5	4,67	0,49
118	O00339	Matrilin-2	MATN2	106,8	6,27	0,52
119	P55145	Mesencephalic astrocyte-derived neurotrophic factor	MANF	20,7	8,69	3,00

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs.* NNMT
120	O94776	Metastasis-associated protein MTA2	MTA2	75,0	9,66	0,43
121	Q9NZL9	Methionine adenosyltransferase 2 subunit beta	MAT2B	37,5	7,36	0,62
122	Q9NX63	MIC complex subunit MIC19	CHCHD3	26,1	8,28	0,42
123	Q66K74	Microtubule-associated protein 1S	MAP1S	112,1	7,30	0,64
124	O43615	Mitochondrial import inner membrane translocase subunit TIM44	TIMM44	51,3	8,32	hoch
125	Q15785	Mitochondrial import receptor subunit TOM34	TOMM34	34,5	8,98	runter
126	O96008	Mitochondrial import receptor subunit TOM40 homolog	TOMM40	37,9	7,25	1,77
127	Q9Y6D9	Mitotic spindle assembly checkpoint protein MAD1	MAD1L1	83,0	5,92	2,00
128	O43148	mRNA cap guanine-N7 methyltransferase	RNMT	54,8	6,61	1,68
129	Q9UJ70	N-acetyl-D-glucosamine kinase	NAGK	37,4	6,24	runter
130	P49821	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	50,8	8,21	runter
131	O75489	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	30,2	7,50	runter
132	P00387	NADH-cytochrome b5 reductase 3	CYB5R3	34,2	7,59	2,42
133	Q9BXJ9	N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	101,2	7,42	1,93
134	Q8TBC4	NEDD8-activating enzyme E1 catalytic subunit	UBA3	51,8	5,45	0,61
135	Q9UMX5	Neudesin	NENF	18,8	5,69	0,66
136	Q9BYT8	Neurolysin, mitochondrial	NLN	80,6	6,64	2,55
137	**P40261**	**Nicotinamide N-methyltransferase**	**NNMT**	**29,6**	**5,74**	**30,34**
138	Q15155	Nodal modulator 1	NOMO1	134,2	5,81	0,50
139	Q5JPE7	Nodal modulator 2	NOMO2	139,4	5,76	0,45
140	P69849	Nodal modulator 3	NOMO3	134,0	5,67	0,45
141	Q9NVX2	Notchless protein homolog 1	NLE1	53,3	7,34	hoch
142	P57740	Nuclear pore complex protein Nup107	NUP107	106,3	5,43	5,43
143	P35658	Nuclear pore complex protein Nup214	NUP214	213,5	7,47	hoch
144	P17480	Nucleolar transcription factor 1	UBTF	89,4	5,81	0,60
145	Q9NX40	OCIA domain-containing protein 1	OCIAD1	27,6	7,49	runter
146	Q56VL3	OCIA domain-containing protein 2	OCIAD2	16,9	9,03	0,61
147	Q9NQR4	Omega-amidase NIT2	NIT2	30,6	7,21	0,61
148	Q8WXF1	Paraspeckle component 1	PSPC1	58,7	6,67	hoch
149	P30405	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	PPIF	22,0	9,38	0,45
150	Q96AY3	Peptidyl-prolyl cis-trans isomerase FKBP10	FKBP10	64,2	5,62	0,47
151	Q9NSD9	Phenylalanine--tRNA ligase beta subunit	FARSB	66,1	6,84	0,50
152	O95394	Phosphoacetylglucosamine mutase	PGM3	59,8	6,25	1,52
153	Q14558	Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	39,4	7,20	2,80
154	P78330	Phosphoserine phosphatase	PSPH	25,0	5,69	hoch

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs.* NNMT
155	Q9HBI6	Phylloquinone omega-hydroxylase CYP4F11	CYP4F11	60,1	6,73	1,56
156	Q9H074	Polyadenylate-binding protein-interacting protein 1	PAIP1	53,5	4,81	0,55
157	Q9UHG3	Prenylcysteine oxidase 1	PCYOX1	56,6	6,18	0,65
158	Q8IY81	pre-rRNA processing protein FTSJ3	FTSJ3	96,5	8,40	1,66
159	Q2NL82	Pre-rRNA-processing protein TSR1 homolog	TSR1	91,8	7,42	runter
160	Q8N0Y7	Probable phosphoglycerate mutase 4	PGAM4	28,8	6,65	1,65
161	O15460	Prolyl 4-hydroxylase subunit alpha-2	P4HA2	60,9	5,71	0,65
162	Q9H7Z7	Prostaglandin E synthase 2	PTGES2	41,9	9,16	runter
163	P49720	Proteasome subunit beta type-3	PSMB3	22,9	6,55	3,87
164	Q5VYK3	Proteasome-associated protein ECM29 homolog	ECM29	204,2	7,12	1,55
165	Q9BT09	Protein canopy homolog 3	CNPY3	30,7	5,49	hoch
166	P17252	Protein kinase C alpha type	PRKCA	76,7	7,05	0,46
167	P05771	Protein kinase C beta type	PRKCB	76,8	7,01	0,52
168	Q8IWE2	Protein NOXP20	FAM114A1	60,7	4,68	0,64
169	Q9BVG4	Protein PBDC1	PBDC1	26,0	4,79	0,66
170	P35813	Protein phosphatase 1A	PPM1A	42,4	5,36	1,56
171	Q15437	Protein transport protein Sec23B	SEC23B	86,4	6,89	2,58
172	Q9H3U1	Protein unc-45 homolog A	UNC45A	103,0	6,07	0,32
173	P22061	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	24,6	7,21	2,38
174	P00734	Prothrombin	F2	70,0	5,90	0,49
175	P06454	Prothymosin alpha	PTMA	12,2	3,78	0,30
176	Q9UBP9	PTB domain-containing engulfment adapter protein 1	GULP1	34,5	7,90	0,35
177	Q9HCE1	Putative helicase MOV-10	MOV10	113,6	8,82	hoch
178	Q2TB90	Putative hexokinase HKDC1	HKDC1	102,5	7,12	0,45
179	Q9Y383	Putative RNA-binding protein Luc7-like 2	LUC7L2	46,5	10,01	0,56
180	Q6P996	Pyridoxal-dependent decarboxylase domain-containing protein 1	PDXDC1	86,7	5,38	0,25
181	P35241	Radixin	RDX	68,5	6,37	0,61
182	Q9H6Z4	Ran-binding protein 3	RANBP3	60,2	4,78	hoch
183	P61006	Ras-related protein Rab-8A	RAB8A	23,7	9,07	0,16
184	P11234	Ras-related protein Ral-B	RALB	23,4	6,62	1,56
185	P61224	Ras-related protein Rap-1b	RAP1B	20,8	5,78	0,52
186	A6NIZ1	Ras-related protein Rap-1b-like protein	2 SV	20,9	5,48	0,52
187	Q15293	Reticulocalbin-1	RCN1	38,9	5,00	0,63
188	Q14257	Reticulocalbin-2	RCN2	36,9	4,40	0,49
189	Q9NQC3	Reticulon-4	RTN4	129,9	4,50	2,55
190	Q92974	Rho guanine nucleotide exchange factor 2	ARHGEF2	111,5	7,27	0,60
191	Q99575	Ribonucleases P/MRP protein subunit POP1	POP1	114,6	9,22	runter

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs.* NNMT
192	Q9Y3A5	Ribosome maturation protein SBDS	SBDS	28,7	8,75	0,61
193	A0AV96	RNA-binding protein 47	RBM47	64,1	7,68	0,57
194	Q5JTH9	RRP12-like protein	RRP12	143,6	8,75	4,94
195	Q15424	Scaffold attachment factor B1	SAFB	102,6	5,47	0,62
196	Q8WVM8	Sec1 family domain-containing protein 1	SCFD1	72,3	6,27	hoch
197	Q92599	Septin-8	39692	55,7	6,28	0,35
198	P84103	Serine/arginine-rich splicing factor 3	SRSF3	19,3	11,65	0,44
199	Q13247	Serine/arginine-rich splicing factor 6	SRSF6	39,6	11,43	2,91
200	Q16629	Serine/arginine-rich splicing factor 7	SRSF7	27,4	11,82	runter
201	Q13177	Serine/threonine-protein kinase PAK 2	PAK2	58,0	5,96	0,57
202	P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	PPP2R2A	51,7	6,20	0,64
203	P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	65,3	5,11	1,77
204	P50454	Serpin H1	SERPINH1	46,4	8,69	0,66
205	Q15165	Serum paraoxonase/arylesterase 2	PON2	39,4	5,60	0,47
206	P61011	Signal recognition particle 54 kDa protein	SRP54	55,7	8,75	2,73
207	O76094	Signal recognition particle subunit SRP72	SRP72	74,6	9,26	3,55
208	O60493	Sorting nexin-3	SNX3	18,8	8,66	runter
209	P63208	S-phase kinase-associated protein 1	SKP1	18,6	4,54	0,43
210	Q14683	Structural maintenance of chromosomes protein 1A	SMC1A	143,1	7,64	1,61
211	Q9NTJ3	Structural maintenance of chromosomes protein 4	SMC4	147,1	6,79	0,66
212	Q96I99	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	46,5	6,39	0,53
213	Q969G3	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	SMARCE1	46,6	4,88	0,16
214	Q96A49	Synapse-associated protein 1	SYAP1	39,9	4,53	runter
215	O00161	Synaptosomal-associated protein 23	SNAP23	23,3	5,01	1,56
216	Q12846	Syntaxin-4	STX4	34,2	6,28	hoch
217	O00560	Syntenin-1	SDCBP	32,4	7,53	0,62
218	P52888	Thimet oligopeptidase	THOP1	78,8	6,05	1,80
219	O43396	Thioredoxin-like protein 1	TXNL1	32,2	4,96	0,63
220	P07204	Thrombomodulin	THBD	60,3	4,92	0,63
221	P62328	Thymosin beta-4	TMSB4X	5,1	5,06	0,57
222	Q9Y2W1	Thyroid hormone receptor-associated protein 3	THRAP3	108,6	10,15	0,56
223	O14776	Transcription elongation regulator 1	TCERG1	123,8	8,65	0,27
224	P20290	Transcription factor BTF3	BTF3	22,2	9,38	0,56
225	Q86YP4	Transcriptional repressor p66-alpha	GATAD2A	68,0	9,94	hoch
226	O43493	Trans-Golgi network integral membrane protein 2	TGOLN2	51,1	5,73	0,65

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs.* NNMT
227	Q99598	Translin-associated protein X	TSNAX	33,1	6,55	0,46
228	Q9HD45	Transmembrane 9 superfamily member 3	TM9SF3	67,8	7,21	1,73
229	Q9BTV4	Transmembrane protein 43	TMEM43	44,8	8,13	0,31
230	Q9Y5L0	Transportin-3	TNPO3	104,1	5,57	0,24
231	P29144	Tripeptidyl-peptidase 2	TPP2	138,3	6,32	0,64
232	Q9Y3I0	tRNA-splicing ligase RtcB homolog	RTCB	55,2	7,23	0,66
233	P09493	Tropomyosin alpha-1 chain	TPM1	32,7	4,74	1,69
234	Q9NRH3	Tubulin gamma-2 chain	TUBG2	51,1	5,80	0,66
235	Q9BTW9	Tubulin-specific chaperone D	TBCD	132,5	6,19	0,45
236	P09012	U1 small nuclear ribonucleoprotein A	SNRPA	31,3	9,83	runter
237	Q14694	Ubiquitin carboxyl-terminal hydrolase 10	USP10	87,1	5,31	0,49
238	Q93009	Ubiquitin carboxyl-terminal hydrolase 7	USP7	128,2	5,55	0,62
239	Q14376	UDP-glucose 4-epimerase	GALE	38,3	6,73	1,69
240	Q8NBZ7	UDP-glucuronic acid decarboxylase 1	UXS1	47,5	8,94	1,56
241	Q16222	UDP-N-acetylhexosamine pyrophosphorylase	UAP1	58,7	6,33	0,45
242	O00159	Unconventional myosin-Ic	MYO1C	121,6	9,41	1,60
243	Q9UM54	Unconventional myosin-VI	MYO6	149,6	8,53	3,67
244	P54725	UV excision repair protein RAD23 homolog A	RAD23A	39,6	4,58	0,64
245	O75351	Vacuolar protein sorting-associated protein 4B	VPS4B	49,3	7,23	1,83
246	Q9P035	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3	HACD3	43,1	8,94	1,64
247	Q9GZS3	WD repeat-containing protein 61	WDR61	33,6	5,47	runter
248	Q2TAY7	WD40 repeat-containing protein SMU1	SMU1	57,5	7,18	hoch
249	Q7Z739	YTH domain-containing family protein 3	YTHDF3	63,8	9,04	runter

Tabelle S6: Differenziell exprimierte Proteine von transient transfizierten Caki-2 Zellen bei 20 µM Methionin (mock *vs*. NNMT)

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
1	Q9BV57	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	ADI1	21,5	5,68	hoch
2	Q9NRX4	14 kDa phosphohistidine phosphatase	PHPT1	13,8	6,07	1,61
3	Q9Y6K5	2'-5'-oligoadenylate synthase 3	OAS3	121,1	8,40	1,59
4	O75832	26S proteasome non-ATPase regulatory subunit 10	PSMD10	24,4	6,10	2,72
5	P55036	26S proteasome non-ATPase regulatory subunit 4	PSMD4	40,7	4,79	0,57
6	P51665	26S proteasome non-ATPase regulatory subunit 7	PSMD7	37,0	6,77	runter
7	Q9BRJ2	39S ribosomal protein L45, mitochondrial	MRPL45	35,3	9,03	hoch
8	P25325	3-mercaptopyruvate sulfurtransferase	MPST	33,2	6,60	hoch
9	P62841	40S ribosomal protein S15	RPS15	17,0	10,39	3,22

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
10	P08708	40S ribosomal protein S17	RPS17	15,5	9,85	1,71
11	P63220	40S ribosomal protein S21	RPS21	9,1	8,50	1,50
12	Q8TD47	40S ribosomal protein S4, Y isoform 2	RPS4Y2	29,3	10,08	1,90
13	Q9BRK5	45 kDa calcium-binding protein	SDF4	41,8	4,86	1,53
14	P49189	4-trimethylaminobutyraldehyde dehydrogenase	ALDH9A1	53,8	5,87	1,87
15	P62750	60S ribosomal protein L23a	RPL23A	17,7	10,45	0,54
16	P61254	60S ribosomal protein L26	RPL26	17,2	10,55	1,54
17	P62910	60S ribosomal protein L32	RPL32	15,9	11,33	2,08
18	O95336	6-phosphogluconolactonase	PGLS	27,5	6,05	1,52
19	Q99798	Aconitate hydratase, mitochondrial	ACO2	85,4	7,61	1,81
20	P68032	Actin, alpha cardiac muscle 1	ACTC1	42,0	5,39	2,02
21	P68133	Actin, alpha skeletal muscle	ACTA1	42,0	5,39	2,02
22	P62736	Actin, aortic smooth muscle	ACTA2	42,0	5,39	2,02
23	P63267	Actin, gamma-enteric smooth muscle	ACTG2	41,9	5,48	2,02
24	O15144	Actin-related protein 2/3 complex subunit 2	ARPC2	34,3	7,36	2,07
25	O95433	Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	38,3	5,53	1,89
26	P55263	Adenosine kinase	ADK	40,5	6,70	runter
27	P54819	Adenylate kinase 2, mitochondrial	AK2	26,5	7,81	0,34
28	P12235	ADP/ATP translocase 1	SLC25A4	33,0	9,76	0,63
29	P12236	ADP/ATP translocase 3	SLC25A6	32,8	9,74	0,65
30	P84077	ADP-ribosylation factor 1	ARF1	20,7	6,80	0,50
31	P61204	ADP-ribosylation factor 3	ARF3	20,6	7,43	0,50
32	Q8N6H7	ADP-ribosylation factor GTPase-activating protein 2	ARFGAP2	56,7	7,99	1,55
33	Q02952	A-kinase anchor protein 12	AKAP12	191,4	4,41	0,65
34	Q04828	Aldo-keto reductase family 1 member C1	AKR1C1	36,8	7,88	0,49
35	P52895	Aldo-keto reductase family 1 member C2	AKR1C2	36,7	7,49	0,59
36	Q01433	AMP deaminase 2	AMPD2	100,6	6,93	1,81
37	Q9BXS5	AP-1 complex subunit mu-1	AP1M1	48,6	7,30	runter
38	O94973	AP-2 complex subunit alpha-2	AP2A2	103,9	6,96	0,55
39	Q9ULZ3	Apoptosis-associated speck-like protein containing a CARD	PYCARD	21,6	6,34	0,50
40	P04424	Argininosuccinate lyase	ASL	51,6	6,48	runter
41	P08243	Asparagine synthetase [glutamine-hydrolyzing]	ASNS	64,3	6,86	0,56
42	O43776	Asparagine--tRNA ligase, cytoplasmic	NARS	62,9	6,25	0,54
43	Q15121	Astrocytic phosphoprotein PEA-15	A15	15,0	5,02	0,64
44	Q9NVI7	ATPase family AAA domain-containing protein 3A	ATAD3A	71,3	8,98	0,58
45	Q5T2N8	ATPase family AAA domain-containing protein 3C	ATAD3C	46,4	9,31	0,33
46	P61221	ATP-binding cassette sub-family E member 1	ABCE1	67,3	8,34	0,65

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
47	Q08211	ATP-dependent RNA helicase A	DHX9	140,9	6,84	0,64
48	Q9NUU7	ATP-dependent RNA helicase DDX19A	DDX19A	53,9	6,58	runter
49	Q9UMR2	ATP-dependent RNA helicase DDX19B	DDX19B	53,9	6,30	runter
50	O75531	Barrier-to-autointegration factor	BANF1	10,1	6,09	2,30
51	Q9Y6E2	Basic leucine zipper and W2 domain-containing protein 2	BZW2	48,1	6,68	runter
52	Q9NYF8	Bcl-2-associated transcription factor 1	BCLAF1	106,1	9,98	0,38
53	P42025	Beta-centractin	ACTR1B	42,3	6,40	0,55
54	Q8IWX8	Calcium homeostasis endoplasmic reticulum protein	CHERP	103,6	9,04	5,73
55	Q13557	Calcium/calmodulin-dependent protein kinase type II subunit delta	CAMK2D	56,3	7,25	2,29
56	O75746	Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	74,7	8,38	hoch
57	Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	74,1	8,62	1,57
58	Q6NUK1	Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	53,3	6,33	1,80
59	Q05682	Caldesmon	CALD1	93,2	5,66	runter
60	P27824	Calnexin	CANX	67,5	4,60	0,66
61	P04632	Calpain small subunit 1	CAPNS1	28,3	5,20	1,60
62	P20810	Calpastatin	CAST	76,5	5,07	1,52
63	P13861	cAMP-dependent protein kinase type II-alpha regulatory subunit	PRKAR2A	45,5	5,07	hoch
64	O75828	Carbonyl reductase [NADPH] 3	CBR3	30,8	6,18	1,98
65	O75976	Carboxypeptidase D	CPD	152,8	6,05	2,74
66	O75718	Cartilage-associated protein	CRTAP	46,5	5,73	3,17
67	P67870	Casein kinase II subunit beta	CSNK2B	24,9	5,55	0,34
68	Q9BXW7	Cat eye syndrome critical region protein 5	CECR5	46,3	8,13	hoch
69	P04040	Catalase	CAT	59,7	7,39	2,00
70	P21964	Catechol O-methyltransferase	COMT	30,0	5,47	0,64
71	Q5ZPR3	CD276 antigen	CD276	57,2	4,91	0,32
72	Q9Y5K6	CD2-associated protein	CD2AP	71,4	6,40	1,58
73	P32970	CD70 antigen	CD70	21,1	8,53	0,65
74	P62633	Cellular nucleic acid-binding protein	CNBP	19,5	7,71	1,71
75	O60271	C-Jun-amino-terminal kinase-interacting protein 4	SPAG9	146,1	5,15	0,64
76	O43809	Cleavage and polyadenylation specificity factor subunit 5	NUDT21	26,2	8,82	hoch
77	Q16630	Cleavage and polyadenylation specificity factor subunit 6	CPSF6	59,2	7,15	0,65
78	O96005	Cleft lip and palate transmembrane protein 1	CLPTM1	76,0	6,30	0,51
79	Q14019	Coactosin-like protein	COTL1	15,9	5,67	0,40
80	P35606	Coatomer subunit beta'	COPB2	102,4	5,27	0,64
81	Q96CT7	Coiled-coil domain-containing protein 124	CCDC124	25,8	9,54	1,55
82	Q96A33	Coiled-coil domain-containing protein 47	CCDC47	55,8	4,87	0,60

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
83	Q8IVM0	Coiled-coil domain-containing protein 50	CCDC50	35,8	6,65	1,63
84	Q16204	Coiled-coil domain-containing protein 6	CCDC6	53,3	7,34	0,56
85	Q9NZB2	Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	121,8	8,88	0,63
86	Q9UBG0	C-type mannose receptor 2	MRC2	166,6	5,83	runter
87	Q92879	CUGBP Elav-like family member 1	CELF1	52,0	8,46	1,87
88	Q5JTJ3	Cytochrome c oxidase assembly factor 6 homolog	COA6	14,1	8,25	hoch
89	P10606	Cytochrome c oxidase subunit 5B, mitochondrial	COX5B	13,7	8,81	1,75
90	P08574	Cytochrome c1, heme protein, mitochondrial	CYC1	35,4	9,00	1,60
91	P21399	Cytoplasmic aconitate hydratase	ACO1	98,3	6,68	1,78
92	Q7L576	Cytoplasmic FMR1-interacting protein 1	CYFIP1	145,1	6,90	1,52
93	Q07065	Cytoskeleton-associated protein 4	CKAP4	66,0	5,92	0,52
94	Q14008	Cytoskeleton-associated protein 5	CKAP5	225,4	7,80	3,74
95	O43175	D-3-phosphoglycerate dehydrogenase	PHGDH	56,6	6,71	2,39
96	Q5BKZ1	DBIRD complex subunit ZNF326	ZNF326	65,6	5,15	1,56
97	P49366	Deoxyhypusine synthase	DHPS	40,9	5,36	1,63
98	P33316	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial	DUT	26,5	9,36	2,01
99	Q9NR28	Diablo homolog, mitochondrial	DIABLO	27,1	5,90	hoch
100	P25205	DNA replication licensing factor MCM3	MCM3	90,9	5,77	0,66
101	P11388	DNA topoisomerase 2-alpha	TOP2A	174,3	8,72	runter
102	P78527	DNA-dependent protein kinase catalytic subunit	PRKDC	468,8	7,12	0,61
103	Q96EY1	DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	52,5	9,26	3,15
104	Q9UBS4	DnaJ homolog subfamily B member 11	DNAJB11	40,5	6,18	1,60
105	Q8IXB1	DnaJ homolog subfamily C member 10	DNAJC10	91,0	7,18	0,48
106	Q99543	DnaJ homolog subfamily C member 2	DNAJC2	72,0	8,70	1,62
107	Q08477	Docosahexaenoic acid omega-hydroxylase CYP4F3	CYP4F3	59,8	7,64	0,41
108	O60762	Dolichol-phosphate mannosyltransferase subunit 1	DPM1	29,6	9,57	0,62
109	Q02750	Dual specificity mitogen-activated protein kinase kinase 1	MAP2K1	43,4	6,62	0,25
110	P36507	Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	44,4	6,55	0,52
111	P51452	Dual specificity protein phosphatase 3	DUSP3	20,5	7,80	0,36
112	Q9UJW0	Dynactin subunit 4	DCTN4	52,3	7,34	0,56
113	P63167	Dynein light chain 1, cytoplasmic	DYNLL1	10,4	7,40	1,85
114	Q9UNE7	E3 ubiquitin-protein ligase CHIP	STUB1	34,8	5,87	0,26
115	Q63HN8	E3 ubiquitin-protein ligase RNF213	RNF213	591,0	6,48	2,45
116	O94874	E3 UFM1-protein ligase 1	UFL1	89,5	6,79	runter
117	Q96C19	EF-hand domain-containing protein D2	EFHD2	26,7	5,20	2,35
118	Q9NZN4	EH domain-containing protein 2	EHD2	61,1	6,46	0,64
119	Q05639	Elongation factor 1-alpha 2	EEF1A2	50,4	9,03	1,67

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
120	P14625	Endoplasmin	HSP90B1	92,4	4,84	0,65
121	P84090	Enhancer of rudimentary homolog	ERH	12,3	5,92	1,68
122	P29323	Ephrin type-B receptor 2	EPHB2	117,4	6,55	1,57
123	P42566	Epidermal growth factor receptor substrate 15	EPS15	98,6	4,64	runter
124	Q9UBC2	Epidermal growth factor receptor substrate 15-like 1	EPS15L1	94,2	5,11	1,83
125	Q8IYD1	Eukaryotic peptide chain release factor GTP-binding subunit ERF3B	GSPT2	68,8	5,43	1,54
126	O00303	Eukaryotic translation initiation factor 3 subunit F	EIF3F	37,5	5,45	runter
127	Q9UBQ5	Eukaryotic translation initiation factor 3 subunit K	EIF3K	25,0	4,93	11,09
128	P06730	Eukaryotic translation initiation factor 4E	EIF4E	25,1	6,15	0,13
129	Q15056	Eukaryotic translation initiation factor 4H	EIF4H	27,4	7,23	2,24
130	P55010	Eukaryotic translation initiation factor 5	EIF5	49,2	5,58	1,57
131	O60841	Eukaryotic translation initiation factor 5B	EIF5B	138,7	5,49	0,52
132	P56537	Eukaryotic translation initiation factor 6	EIF6	26,6	4,68	0,61
133	Q9Y2L1	Exosome complex exonuclease RRP44	DIS3	108,9	7,14	runter
134	Q9UIA9	Exportin-7	XPO7	123,8	6,32	0,66
135	P51648	Fatty aldehyde dehydrogenase	ALDH3A2	54,8	7,88	0,59
136	P30043	Flavin reductase (NADPH)	BLVRB	22,1	7,65	1,77
137	Q13642	Four and a half LIM domains protein 1	FHL1	36,2	8,97	runter
138	P51570	Galactokinase	GALK1	42,2	6,46	2,02
139	Q9UEY8	Gamma-adducin	ADD3	79,1	6,32	hoch
140	O60763	General vesicular transport factor p115	USO1	107,8	4,91	0,66
141	P60983	Glia maturation factor beta	GMFB	16,7	5,29	hoch
142	P46926	Glucosamine-6-phosphate isomerase 1	GNPDA1	32,6	6,92	3,87
143	P14314	Glucosidase 2 subunit beta	PRKCSH	59,4	4,41	1,57
144	P48506	Glutamate--cysteine ligase catalytic subunit	GCLC	72,7	6,09	1,92
145	Q9BQ67	Glutamate-rich WD repeat-containing protein 1	GRWD1	49,4	4,92	runter
146	P13807	Glycogen [starch] synthase, muscle	GYS1	83,7	6,18	0,28
147	P30419	Glycylpeptide N-tetradecanoyltransferase 1	NMT1	56,8	7,80	0,53
148	Q96S52	GPI transamidase component PIG-S	PIGS	61,6	6,49	runter
149	Q12849	G-rich sequence factor 1	GRSF1	53,1	6,19	1,94
150	Q99988	Growth/differentiation factor 15	GDF15	34,1	9,66	1,84
151	Q9HAV7	GrpE protein homolog 1, mitochondrial	GRL1	24,3	8,12	2,52
152	P01112	GTPase HRas	HRAS	21,3	5,31	3,29
153	P01111	GTPase NRas	NRAS	21,2	5,17	2,87
154	P63092	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	GNAS	45,6	5,82	1,59

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
155	Q5JWF2	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	111,0	5,03	1,59
156	Q9HAV0	Guanine nucleotide-binding protein subunit beta-4	GNB4	37,5	6,00	runter
157	O95757	Heat shock 70 kDa protein 4L	HSPA4L	94,5	5,88	1,80
158	P08581	Hepatocyte growth factor receptor	MET	155,4	7,33	0,52
159	P51858	Hepatoma-derived growth factor	HDGF	26,8	4,73	1,68
160	P52597	Heterogeneous nuclear ribonucleoprotein F	HNRNPF	45,6	5,58	1,51
161	P55795	Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	49,2	6,30	1,55
162	P52272	Heterogeneous nuclear ribonucleoprotein M	HNRNPM	77,5	8,70	1,51
163	O15347	High mobility group protein B3	HMGB3	23,0	8,37	hoch
164	P52926	High mobility group protein HMGI-C	HMGA2	11,8	10,62	1,51
165	Q92769	Histone deacetylase 2	HDAC2	55,3	5,91	0,59
166	Q92522	Histone H1x	H1FX	22,5	10,76	hoch
167	Q6FI13	Histone H2A type 2-A	HIST2H2AA3	14,1	10,90	2,15
168	Q16777	Histone H2A type 2-C	HIST2H2AC	14,0	10,90	2,15
169	P68431	Histone H3.1	HIST1H3A	15,4	11,12	0,35
170	Q71DI3	Histone H3.2	HIST2H3A	15,4	11,27	0,25
171	P84243	Histone H3.3	H3F3A	15,3	11,27	0,34
172	Q09028	Histone-binding protein RBBP4	RBBP4	47,6	4,89	0,33
173	Q16543	Hsp90 co-chaperone Cdc37	CDC37	44,4	5,25	1,72
174	O75146	Huntingtin-interacting protein 1-related protein	HIP1R	119,3	6,67	hoch
175	Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HADH	34,3	8,85	1,51
176	P52294	Importin subunit alpha-5	KPNA1	60,2	5,01	runter
177	O60684	Importin subunit alpha-7	KPNA6	60,0	4,98	0,57
178	O00410	Importin-5	IPO5	123,6	4,94	0,57
179	Q96P70	Importin-9	IPO9	115,9	4,81	0,46
180	P36268	Inactive gamma-glutamyltranspeptidase 2	GGT2	61,7	7,58	hoch
181	P80217	Interferon-induced 35 kDa protein	IFI35	31,5	6,09	1,64
182	P48735	Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	50,9	8,69	2,13
183	P41252	Isoleucine--tRNA ligase, cytoplasmic	IARS	144,4	6,15	0,57
184	Q07866	Kinesin light chain 1	KLC1	65,3	6,20	2,31
185	Q9H0B6	Kinesin light chain 2	KLC2	68,9	7,15	hoch
186	P33176	Kinesin-1 heavy chain	KIF5B	109,6	6,51	1,81
187	P42166	Lamina-associated polypeptide 2, isoform alpha	TMPO	75,4	7,66	2,00
188	P09960	Leukotriene A-4 hydrolase	LTA4H	69,2	6,18	0,66
189	O60488	Long-chain-fatty-acid--CoA ligase 4	ACSL4	79,1	8,38	runter
190	P10253	Lysosomal alpha-glucosidase	GAA	105,3	6,00	2,45
191	Q14108	Lysosome membrane protein 2	SCARB2	54,3	5,14	0,54

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
192	P34949	Mannose-6-phosphate isomerase	MPI	46,6	5,95	1,55
193	O94776	Metastasis-associated protein MTA2	MTA2	75,0	9,66	9,95
194	O75431	Metaxin-2	MTX2	29,7	6,29	runter
195	P50579	Methionine aminopeptidase 2	METAP2	52,9	5,82	1,52
196	Q9NX63	MIC complex subunit MIC19	CHCHD3	26,1	8,28	3,44
197	Q66K74	Microtubule-associated protein 1S	MAP1S	112,1	7,30	0,61
198	P21741	Midkine	MDK	15,6	9,79	1,53
199	Q96T76	MMS19 nucleotide excision repair protein homolog	MMS19	113,2	6,35	0,34
200	Q9BQG0	Myb-binding protein 1A	MYBBP1A	148,8	9,28	2,09
201	Q9Y6M9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	NDUFB9	21,8	8,38	runter
202	P49821	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	50,8	8,21	2,15
203	P22570	NADPH:adrenodoxin oxidoreductase, mitochondrial	FDXR	53,8	8,44	1,61
204	Q9BXJ9	N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	101,2	7,42	2,28
205	Q9GZZ1	N-alpha-acetyltransferase 50	NAA50	19,4	8,81	runter
206	Q13564	NEDD8-activating enzyme E1 regulatory subunit	NAE1	60,2	5,40	0,49
207	Q9BYT8	Neurolysin, mitochondrial	NLN	80,6	6,64	1,55
208	Q9Y639	Neuroplastin	NPTN	44,4	7,99	1,69
209	Q96TA1	Niban-like protein 1	FAM129B	84,1	6,19	0,66
210	**P40261**	**Nicotinamide N-methyltransferase**	**NNMT**	**29,6**	**5,74**	**36,73**
211	Q13287	N-myc-interactor	NMI	35,0	5,34	hoch
212	Q15155	Nodal modulator 1	NOMO1	134,2	5,81	0,44
213	Q5JPE7	Nodal modulator 2	NOMO2	139,4	5,76	0,44
214	P69849	Nodal modulator 3	NOMO3	134,0	5,67	0,44
215	P22307	Non-specific lipid-transfer protein	SCP2	59,0	6,89	hoch
216	Q09161	Nuclear cap-binding protein subunit 1	NCBP1	91,8	6,43	2,09
217	Q00653	Nuclear factor NF-kappa-B p100 subunit	NFKB2	96,7	6,25	1,69
218	Q9Y266	Nuclear migration protein nudC	NUDC	38,2	5,38	1,80
219	Q14980	Nuclear mitotic apparatus protein 1	NUMA1	238,1	5,78	1,50
220	O75694	Nuclear pore complex protein Nup155	NUP155	155,1	6,16	0,50
221	Q92621	Nuclear pore complex protein Nup205	NUP205	227,8	6,19	0,55
222	P35658	Nuclear pore complex protein Nup214	NUP214	213,5	7,47	0,33
223	Q8N1F7	Nuclear pore complex protein Nup93	NUP93	93,4	5,72	2,16
224	Q02818	Nucleobindin-1	NUCB1	53,8	5,25	2,28
225	P80303	Nucleobindin-2	NUCB2	50,2	5,12	1,52
226	P15531	Nucleoside diphosphate kinase A	NME1	17,1	6,19	1,50
227	Q9NQR4	Omega-amidase NIT2	NIT2	30,6	7,21	0,30

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
228	Q9BUP3	Oxidoreductase HTATIP2	HTATIP2	27,0	8,38	2,39
229	Q9BZF1	Oxysterol-binding protein-related protein 8	OSBPL8	101,1	6,96	1,55
230	O75475	PC4 and SFRS1-interacting protein	PSIP1	60,1	9,13	hoch
231	O00151	PDZ and LIM domain protein 1	PDLIM1	36,0	7,02	1,50
232	O14908	PDZ domain-containing protein GIPC1	GIPC1	36,0	6,28	4,88
233	Q08752	Peptidyl-prolyl cis-trans isomerase D	PPID	40,7	7,21	0,58
234	Q96AY3	Peptidyl-prolyl cis-trans isomerase FKBP10	FKBP10	64,2	5,62	0,38
235	O95302	Peptidyl-prolyl cis-trans isomerase FKBP9	FKBP9	63,0	5,08	0,48
236	Q9Y237	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	PIN4	13,8	9,77	1,52
237	P30044	Peroxiredoxin-5, mitochondrial	PRDX5	22,1	8,70	0,62
238	O95394	Phosphoacetylglucosamine mutase	PGM3	59,8	6,25	1,51
239	Q96G03	Phosphoglucomutase-2	PGM2	68,2	6,73	0,54
240	P15259	Phosphoglycerate mutase 2	PGAM2	28,7	8,88	3,84
241	Q9Y617	Phosphoserine aminotransferase	PSAT1	40,4	7,66	1,70
242	Q9HBI6	Phylloquinone omega-hydroxylase CYP4F11	CYP4F11	60,1	6,73	0,60
243	Q9UKK3	Poly [ADP-ribose] polymerase 4	PARP4	192,5	5,66	0,39
244	P57721	Poly(rC)-binding protein 3	PCBP3	39,4	8,07	0,40
245	Q9BY77	Polymerase delta-interacting protein 3	POLDIP3	46,1	9,99	2,43
246	Q10471	Polypeptide N-acetylgalactosaminyltransferase 2	GALNT2	64,7	8,35	0,63
247	O94906	Pre-mRNA-processing factor 6	PRPF6	106,9	8,25	runter
248	Q15007	Pre-mRNA-splicing regulator WTAP	WTAP	44,2	5,19	runter
249	Q9UHG3	Prenylcysteine oxidase 1	PCYOX1	56,6	6,18	runter
250	Q2NL82	Pre-rRNA-processing protein TSR1 homolog	TSR1	91,8	7,42	runter
251	P46087	Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase	NOP2	89,2	9,23	1,81
252	P26196	Probable ATP-dependent RNA helicase DDX6	DDX6	54,4	8,66	1,88
253	Q8IY21	Probable ATP-dependent RNA helicase DDX60	DDX60	197,7	7,59	0,50
254	Q8N0Y7	Probable phosphoglycerate mutase 4	PGAM4	28,8	6,65	2,30
255	Q14914	Prostaglandin reductase 1	PTGR1	35,8	8,29	1,65
256	P49721	Proteasome subunit beta type-2	PSMB2	22,8	7,02	1,63
257	P28072	Proteasome subunit beta type-6	PSMB6	25,3	4,92	2,19
258	Q99873	Protein arginine N-methyltransferase 1	PRMT1	41,5	5,43	0,46
259	O14744	Protein arginine N-methyltransferase 5	PRMT5	72,6	6,29	2,03
260	Q5TDH0	Protein DDI1 homolog 2	DDI2	44,5	5,05	runter
261	Q96JJ7	Protein disulfide-isomerase TMX3	TMX3	51,8	4,91	runter
262	Q9H0Q0	Protein FAM49A	FAM49A	37,3	6,01	hoch
263	Q8NCA5	Protein FAM98A	FAM98A	55,4	9,03	0,45
264	P17252	Protein kinase C alpha type	PRKCA	76,7	7,05	0,38

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
265	Q9BZQ8	Protein Niban	FAM129A	103,1	4,78	1,63
266	Q9UFN0	Protein NipSnap homolog 3A	NIPSNAP3A	28,4	9,16	runter
267	Q15435	Protein phosphatase 1 regulatory subunit 7	PPP1R7	41,5	4,91	4,03
268	P41236	Protein phosphatase inhibitor 2	PPP1R2	23,0	4,74	1,70
269	Q6NXS1	Protein phosphatase inhibitor 2-like protein 3	PPP1R2P3	23,0	4,92	1,70
270	Q969Z0	Protein TBRG4	TBRG4	70,7	7,42	runter
271	Q15437	Protein transport protein Sec23B	SEC23B	86,4	6,89	4,76
272	P53992	Protein transport protein Sec24C	SEC24C	118,2	7,06	0,66
273	O94855	Protein transport protein Sec24D	SEC24D	112,9	7,25	0,58
274	Q9H3U1	Protein unc-45 homolog A	UNC45A	103,0	6,07	1,68
275	Q9H993	Protein-glutamate O-methyltransferase	ARMT1	51,1	5,76	runter
276	Q14671	Pumilio homolog 1	PUM1	126,4	6,84	hoch
277	Q9NQ29	Putative RNA-binding protein Luc7-like 1	LUC7L	43,7	9,92	hoch
278	O00764	Pyridoxal kinase	PDXK	35,1	6,13	1,53
279	Q6P996	Pyridoxal-dependent decarboxylase domain-containing protein 1	PDXDC1	86,7	5,38	1,91
280	P62491	Ras-related protein Rab-11A	RAB11A	24,4	6,57	1,57
281	Q15907	Ras-related protein Rab-11B	RAB11B	24,5	5,94	1,80
282	P51153	Ras-related protein Rab-13	RAB13	22,8	9,19	0,23
283	P62820	Ras-related protein Rab-1A	RAB1A	22,7	6,21	2,90
284	Q9UL25	Ras-related protein Rab-21	RAB21	24,3	7,94	0,27
285	Q8WUD1	Ras-related protein Rab-2B	RAB2B	24,2	7,83	0,65
286	P51148	Ras-related protein Rab-5C	RAB5C	23,5	8,41	0,64
287	Q92930	Ras-related protein Rab-8B	RAB8B	23,6	9,07	runter
288	P62834	Ras-related protein Rap-1A	RAP1A	21,0	6,67	runter
289	Q9NQG5	Regulation of nuclear pre-mRNA domain-containing protein 1B	RPRD1B	36,9	5,97	1,53
290	P35250	Replication factor C subunit 2	RFC2	39,1	6,44	0,50
291	P15927	Replication protein A 32 kDa subunit	RPA2	29,2	6,15	1,55
292	Q15293	Reticulocalbin-1	RCN1	38,9	5,00	1,53
293	Q9NQC3	Reticulon-4	RTN4	129,9	4,50	0,43
294	Q8IZV5	Retinol dehydrogenase 10	RDH10	38,1	7,40	0,44
295	P08134	Rho-related GTP-binding protein RhoC	RHOC	22,0	6,58	runter
296	P11908	Ribose-phosphate pyrophosphokinase 2	PRPS2	34,7	6,61	0,55
297	P21108	Ribose-phosphate pyrophosphokinase 3	PRPS1L1	34,8	6,35	0,27
298	O76021	Ribosomal L1 domain-containing protein 1	RSL1D1	54,9	10,13	0,39
299	Q15418	Ribosomal protein S6 kinase alpha-1	RPS6KA1	82,7	7,83	runter
300	Q14137	Ribosome biogenesis protein BOP1	BOP1	83,6	6,19	2,07

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
301	Q96E39	RNA binding motif protein, X-linked-like-1	RBMXL1	42,1	9,89	1,57
302	P38159	RNA-binding motif protein, X chromosome	RBMX	42,3	10,05	1,55
303	Q9NTZ6	RNA-binding protein 12	RBM12	97,3	8,63	hoch
304	P98179	RNA-binding protein 3	RBM3	17,2	8,91	2,18
305	Q9BWF3	RNA-binding protein 4	RBM4	40,3	7,08	hoch
306	Q5JTH9	RRP12-like protein	RRP12	143,6	8,75	0,13
307	P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	114,7	5,34	0,60
308	Q92599	Septin-8	39692	55,7	6,28	0,63
309	P83111	Serine beta-lactamase-like protein LACTB, mitochondrial	LACTB	60,7	8,53	hoch
310	O75494	Serine/arginine-rich splicing factor 10	SRSF10	31,3	11,27	hoch
311	P84103	Serine/arginine-rich splicing factor 3	SRSF3	19,3	11,65	1,67
312	Q9P289	Serine/threonine-protein kinase 26	STK26	46,5	5,29	0,42
313	Q13177	Serine/threonine-protein kinase PAK 2	PAK2	58,0	5,96	0,64
314	Q14738	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	69,9	8,13	0,56
315	P53041	Serine/threonine-protein phosphatase 5	PPP5C	56,8	6,28	0,51
316	Q9BRF8	Serine/threonine-protein phosphatase CPPED1	CPD1	35,5	6,20	0,29
317	P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	PPP1CA	37,5	6,33	runter
318	P50454	Serpin H1	SERPINH1	46,4	8,69	1,98
319	Q9Y5M8	Signal recognition particle receptor subunit beta	SRPRB	29,7	9,04	1,66
320	O76094	Signal recognition particle subunit SRP72	SRP72	74,6	9,26	2,44
321	Q92783	Signal transducing adapter molecule 1	STAM	59,1	4,82	1,74
322	Q13573	SNW domain-containing protein 1	SNW1	61,5	9,52	3,56
323	P05026	Sodium/potassium-transporting ATPase subunit beta-1	ATP1B1	35,0	8,53	3,96
324	Q13596	Sorting nexin-1	SNX1	59,0	5,15	2,20
325	Q9NUQ6	SPATS2-like protein	SPATS2L	61,7	9,64	1,80
326	P19623	Spermidine synthase	SRM	33,8	5,49	0,33
327	P63208	S-phase kinase-associated protein 1	SKP1	18,6	4,54	1,98
328	Q13435	Splicing factor 3B subunit 2	SF3B2	100,2	5,67	1,51
329	Q96I25	Splicing factor 45	RBM17	44,9	5,97	0,28
330	Q15020	Squamous cell carcinoma antigen recognized by T-cells 3	SART3	109,9	5,57	1,80
331	Q14683	Structural maintenance of chromosomes protein 1A	SMC1A	143,1	7,64	2,14
332	Q9NTJ3	Structural maintenance of chromosomes protein 4	SMC4	147,1	6,79	runter
333	Q9UH99	SUN domain-containing protein 2	SUN2	80,3	6,73	0,64
334	P42285	Superkiller viralicidic activity 2-like 2	SKIV2L2	117,7	6,52	0,49
335	Q8TAQ2	SWI/SNF complex subunit SMARCC2	SMARCC2	132,8	5,69	1,76

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
336	O60264	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	121,8	8,09	0,62
337	Q969G3	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	SMARCE1	46,6	4,88	0,05
338	O00161	Synaptosomal-associated protein 23	SNAP23	23,3	5,01	3,76
339	Q12846	Syntaxin-4	STX4	34,2	6,28	hoch
340	P52888	Thimet oligopeptidase	THOP1	78,8	6,05	runter
341	P19971	Thymidine phosphorylase	TYMP	49,9	5,53	0,58
342	P62328	Thymosin beta-4	TMSB4X	5,1	5,06	1,99
343	Q15654	Thyroid receptor-interacting protein 6	TRIP6	50,3	7,37	0,45
344	Q07157	Tight junction protein ZO-1	TJP1	195,3	6,70	1,76
345	O75663	TIP41-like protein	TIPRL	31,4	5,91	2,10
346	O14776	Transcription elongation regulator 1	TCERG1	123,8	8,65	13,16
347	P20290	Transcription factor BTF3	BTF3	22,2	9,38	1,73
348	Q96K17	Transcription factor BTF3 homolog 4	BTF3L4	17,3	6,35	1,54
349	Q00577	Transcriptional activator protein Pur-alpha	PURA	34,9	6,44	hoch
350	P61586	Transforming protein RhoA	RHOA	21,8	6,10	1,51
351	O43493	Trans-Golgi network integral membrane protein 2	TGOLN2	51,1	5,73	0,36
352	Q15629	Translocating chain-associated membrane protein 1	TRAM1	43,0	9,63	runter
353	Q9HD45	Transmembrane 9 superfamily member 3	TM9SF3	67,8	7,21	0,26
354	Q3LXA3	Triokinase/FMN cyclase	TKFC	58,9	7,49	0,61
355	Q9Y606	tRNA pseudouridine synthase A, mitochondrial	PUS1	47,4	8,41	runter
356	P07951	Tropomyosin beta chain	TPM2	32,8	4,70	3,35
357	A6NHL2	Tubulin alpha chain-like 3	TUBAL3	49,9	6,05	0,64
358	P04350	Tubulin beta-4A chain	TUBB4A	49,6	4,88	1,72
359	P68371	Tubulin beta-4B chain	TUBB4B	49,8	4,89	hoch
360	P23258	Tubulin gamma-1 chain	TUBG1	51,1	6,14	1,63
361	Q14166	Tubulin--tyrosine ligase-like protein 12	TTLL12	74,4	5,53	runter
362	P25445	Tumor necrosis factor receptor superfamily member 6	FAS	37,7	7,94	2,43
363	Q6IBS0	Twinfilin-2	TWF2	39,5	6,84	0,57
364	Q05209	Tyrosine-protein phosphatase non-receptor type 12	PTPN12	88,1	5,62	hoch
365	O43172	U4/U6 small nuclear ribonucleoprotein Prp4	PRPF4	58,4	7,42	0,21
366	O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	244,4	6,06	0,59
367	Q96DI7	U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	39,3	8,10	1,51
368	P45974	Ubiquitin carboxyl-terminal hydrolase 5	USP5	95,7	5,03	0,65
369	Q93009	Ubiquitin carboxyl-terminal hydrolase 7	USP7	128,2	5,55	0,31
370	Q8TF42	Ubiquitin-associated and SH3 domain-containing protein B	UBASH3B	72,6	6,93	1,80
371	Q13404	Ubiquitin-conjugating enzyme E2 variant 1	UBE2V1	16,5	7,93	0,35

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
372	P05161	Ubiquitin-like protein ISG15	ISG15	17,9	7,44	0,61
373	Q14376	UDP-glucose 4-epimerase	GALE	38,3	6,73	1,65
374	Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1	UGGT1	177,1	5,63	0,61
375	P19224	UDP-glucuronosyltransferase 1-6	UGT1A6	60,7	8,41	1,50
376	Q16222	UDP-N-acetylhexosamine pyrophosphorylase	UAP1	58,7	6,33	0,37
377	Q9UM54	Unconventional myosin-VI	MYO6	149,6	8,53	1,66
378	Q9HB07	UPF0160 protein MYG1, mitochondrial	C12orf10	42,4	6,67	hoch
379	P61421	V-type proton ATPase subunit d 1	ATP6V0D1	40,3	5,00	runter
380	Q8WU90	Zinc finger CCCH domain-containing protein 15	ZC3H15	48,6	5,31	hoch
381	O15231	Zinc finger protein 185	ZNF185	73,5	7,01	1,64

Tabelle S7: Differenziell exprimierte Proteine von transient transfizierten 786-O Zellen bei 100 µM Methionin (sisc *vs*. siNNMT)

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs*. siNNMT
1	Q04446	1,4-alpha-glucan-branching enzyme	GBE1	80,4	6,32	1,58
2	P61604	10 kDa heat shock protein, mitochondrial	HS1	10,9	8,92	0,44
3	Q9NRX4	14 kDa phosphohistidine phosphatase	PHPT1	13,8	6,07	0,49
4	Q04917	14-3-3 protein eta	YWHAH	28,2	4,84	3,10
5	P61981	14-3-3 protein gamma	YWHAG	28,3	4,89	0,49
6	Q16698	2,4-dienoyl-CoA reductase, mitochondrial	DECR1	36,0	9,28	0,58
7	Q9Y6K5	2'-5'-oligoadenylate synthase 3	OAS3	121,1	8,40	runter
8	P43686	26S protease regulatory subunit 6B	PSMC4	47,3	5,21	0,34
9	O75832	26S proteasome non-ATPase regulatory subunit 10	PSMD10	24,4	6,10	1,67
10	O00487	26S proteasome non-ATPase regulatory subunit 14	PSMD14	34,6	6,52	2,22
11	Q13200	26S proteasome non-ATPase regulatory subunit 2	PSMD2	100,1	5,20	1,60
12	P51665	26S proteasome non-ATPase regulatory subunit 7	PSMD7	37,0	6,77	4,50
13	Q9Y676	28S ribosomal protein S18b, mitochondrial	MRPS18B	29,4	9,38	0,66
14	P51398	28S ribosomal protein S29, mitochondrial	DAP3	45,5	8,88	0,60
15	Q9NP92	28S ribosomal protein S30, mitochondrial	MRPS30	50,3	7,97	2,58
16	P82675	28S ribosomal protein S5, mitochondrial	MRPS5	48,0	9,92	0,32
17	Q02218	2-oxoglutarate dehydrogenase, mitochondrial	OGDH	115,9	6,86	0,44
18	O95861	3'(2'),5'-bisphosphate nucleotidase 1	BPNT1	33,4	5,69	runter
19	Q9BYD6	39S ribosomal protein L1, mitochondrial	MRPL1	36,9	8,78	runter
20	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial	HIBADH	35,3	8,13	runter
21	P25325	3-mercaptopyruvate sulfurtransferase	MPST	33,2	6,60	0,53
22	P25398	40S ribosomal protein S12	RPS12	14,5	7,21	0,47

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs.* siNNMT
23	P62263	40S ribosomal protein S14	RPS14	16,3	10,05	0,49
24	P62244	40S ribosomal protein S15a	RPS15A	14,8	10,13	0,46
25	P08708	40S ribosomal protein S17	RPS17	15,5	9,85	0,56
26	P63220	40S ribosomal protein S21	RPS21	9,1	8,50	0,63
27	P42677	40S ribosomal protein S27	RPS27	9,5	9,45	0,66
28	P23396	40S ribosomal protein S3	RPS3	26,7	9,66	0,44
29	P61247	40S ribosomal protein S3a	RPS3A	29,9	9,73	0,58
30	P22090	40S ribosomal protein S4, Y isoform 1	RPS4Y1	29,4	10,24	0,55
31	Q8TD47	40S ribosomal protein S4, Y isoform 2	RPS4Y2	29,3	10,08	1,76
32	Q9BRK5	45 kDa calcium-binding protein	SDF4	41,8	4,86	2,45
33	P49189	4-trimethylaminobutyraldehyde dehydrogenase	ALDH9A1	53,8	5,87	3,19
34	P21589	5'-nucleotidase	NT5E	63,3	7,03	2,57
35	Q5TFE4	5'-nucleotidase domain-containing protein 1	NT5DC1	51,8	6,35	1,98
36	P27635	60S ribosomal protein L10	RPL10	24,6	10,08	0,54
37	P30050	60S ribosomal protein L12	RPL12	17,8	9,42	0,64
38	P40429	60S ribosomal protein L13a	RPL13A	23,6	10,93	0,60
39	P18621	60S ribosomal protein L17	RPL17	21,4	10,17	0,50
40	P62750	60S ribosomal protein L23a	RPL23A	17,7	10,45	2,12
41	P61254	60S ribosomal protein L26	RPL26	17,2	10,55	1,58
42	Q9UNX3	60S ribosomal protein L26-like 1	RPL26L1	17,2	10,55	2,78
43	P46779	60S ribosomal protein L28	RPL28	15,7	12,02	3,47
44	P62888	60S ribosomal protein L30	RPL30	12,8	9,63	0,59
45	Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic	ACAT2	41,3	6,92	1,99
46	P24752	Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	45,2	8,85	0,50
47	P39687	Acidic leucine-rich nuclear phosphoprotein 32 family member A	ANP32A	28,6	4,09	0,45
48	Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B	ANP32B	28,8	4,06	0,62
49	Q9BTT0	Acidic leucine-rich nuclear phosphoprotein 32 family member E	ANP32E	30,7	3,85	0,57
50	P68032	Actin, alpha cardiac muscle 1	ACTC1	42,0	5,39	0,56
51	P68133	Actin, alpha skeletal muscle	ACTA1	42,0	5,39	0,56
52	P62736	Actin, aortic smooth muscle	ACTA2	42,0	5,39	0,56
53	P63267	Actin, gamma-enteric smooth muscle	ACTG2	41,9	5,48	0,56
54	Q53H12	Acylglycerol kinase, mitochondrial	AGK	47,1	8,09	0,57
55	P46108	Adapter molecule crk	CRK	33,8	5,55	0,42
56	O43865	Adenosylhomocysteinase 2	AHCYL1	58,9	6,89	0,41
57	P54819	Adenylate kinase 2, mitochondrial	AK2	26,5	7,81	0,53

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58	P00568	Adenylate kinase isoenzyme 1	AK1	21,6	8,63	0,60
59	P62330	ADP-ribosylation factor 6	ARF6	20,1	8,95	runter
60	Q8N6H7	ADP-ribosylation factor GTPase-activating protein 2	ARFGAP2	56,7	7,99	runter
61	O43488	Aflatoxin B1 aldehyde reductase member 2	AKR7A2	39,6	7,17	0,51
62	Q02952	A-kinase anchor protein 12	AKAP12	191,4	4,41	2,09
63	P49588	Alanine--tRNA ligase, cytoplasmic	AARS	106,7	5,53	0,52
64	P14550	Alcohol dehydrogenase [NADP(+)]	AKR1A1	36,6	6,79	0,28
65	Q8IZ83	Aldehyde dehydrogenase family 16 member A1	ALDH16A1	85,1	6,79	runter
66	P05091	Aldehyde dehydrogenase, mitochondrial	ALDH2	56,3	7,05	runter
67	O60218	Aldo-keto reductase family 1 member B10	AKR1B10	36,0	7,84	runter
68	P42330	Aldo-keto reductase family 1 member C3	AKR1C3	36,8	7,94	0,29
69	P15121	Aldose reductase	AKR1B1	35,8	6,98	0,38
70	P30533	Alpha-2-macroglobulin receptor-associated protein	LRPAP1	41,4	8,78	0,22
71	P35609	Alpha-actinin-2	ACTN2	103,8	5,45	3,39
72	Q08043	Alpha-actinin-3	ACTN3	103,2	5,52	runter
73	P35611	Alpha-adducin	ADD1	80,9	5,83	0,51
74	P49419	Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1	58,5	7,99	0,45
75	Q9C0B1	Alpha-ketoglutarate-dependent dioxygenase FTO	FTO	58,2	5,22	runter
76	P05067	Amyloid beta A4 protein	APP	86,9	4,82	0,54
77	Q06481	Amyloid-like protein 2	APLP2	86,9	4,79	runter
78	P50995	Annexin A11	ANXA11	54,4	7,65	0,58
79	P09525	Annexin A4	ANXA4	35,9	6,13	0,58
80	O95782	AP-2 complex subunit alpha-1	AP2A1	107,5	7,03	0,66
81	O14617	AP-3 complex subunit delta-1	AP3D1	130,1	8,48	0,47
82	Q9BZZ5	Apoptosis inhibitor 5	API5	59,0	7,34	runter
83	P52594	Arf-GAP domain and FG repeat-containing protein 1	AGFG1	58,2	8,63	0,53
84	Q9UH62	Armadillo repeat-containing X-linked protein 3	ARMCX3	42,5	8,37	runter
85	P08243	Asparagine synthetase [glutamine-hydrolyzing]	ASNS	64,3	6,86	0,52
86	P17174	Aspartate aminotransferase, cytoplasmic	GOT1	46,2	7,01	0,60
87	Q12797	Aspartyl/asparaginyl beta-hydroxylase	ASPH	85,8	5,01	2,53
88	Q9UBB4	Ataxin-10	ATXN10	53,5	5,25	0,64
89	Q6DD88	Atlastin-3	ATL3	60,5	5,66	1,65
90	O75947	ATP synthase subunit d, mitochondrial	ATP5H	18,5	5,30	0,51
91	P53396	ATP-citrate synthase	ACLY	120,8	7,33	1,71
92	P08237	ATP-dependent 6-phosphofructokinase, muscle type	PFKM	85,1	7,99	runter
93	Q92499	ATP-dependent RNA helicase DDX1	DDX1	82,4	7,23	0,48
94	Q86XP3	ATP-dependent RNA helicase DDX42	DDX42	102,9	7,02	runter

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95	O75531	Barrier-to-autointegration factor	BANF1	10,1	6,09	0,38
96	P35613	Basigin	BSG	42,2	5,66	0,55
97	P51572	B-cell receptor-associated protein 31	BCAP31	28,0	8,44	1,85
98	P61769	Beta-2-microglobulin	B2M	13,7	6,52	0,47
99	Q562R1	Beta-actin-like protein 2	ACTBL2	42,0	5,59	5247,09
100	O95340	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2	PAPSS2	69,5	8,03	0,52
101	P53004	Biliverdin reductase A	BLVRA	33,4	6,44	0,60
102	P80723	Brain acid soluble protein 1	BASP1	22,7	4,63	2,59
103	Q9P287	BRCA2 and CDKN1A-interacting protein	BCCIP	36,0	4,61	0,60
104	Q15018	BRISC complex subunit Abro1	FAM175B	46,9	6,21	runter
105	P27708	CAD protein	CAD	242,8	6,46	0,56
106	O75746	Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	74,7	8,38	0,56
107	Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	74,1	8,62	0,53
108	P04632	Calpain small subunit 1	CAPNS1	28,3	5,20	0,45
109	P07384	Calpain-1 catalytic subunit	CAPN1	81,8	5,67	0,65
110	P17655	Calpain-2 catalytic subunit	CAPN2	79,9	4,98	0,66
111	P20810	Calpastatin	CAST	76,5	5,07	0,63
112	P00918	Carbonic anhydrase 2	CA2	29,2	7,40	0,36
113	P42574	Caspase-3	CASP3	31,6	6,54	runter
114	P35222	Catenin beta-1	CTNNB1	85,4	5,86	0,63
115	P07339	Cathepsin D	CTSD	44,5	6,54	0,59
116	Q13740	CD166 antigen	ALCAM	65,1	6,25	0,48
117	Q9Y5K6	CD2-associated protein	CD2AP	71,4	6,40	0,62
118	Q9H3Q1	Cdc42 effector protein 4	CDC42EP4	38,0	5,19	runter
119	Q99459	Cell division cycle 5-like protein	CDC5L	92,2	8,18	runter
120	P62633	Cellular nucleic acid-binding protein	CNBP	19,5	7,71	0,51
121	Q5SW79	Centrosomal protein of 170 kDa	CEP170	175,2	7,11	runter
122	Q9Y696	Chloride intracellular channel protein 4	CLIC4	28,8	5,59	0,29
123	P83916	Chromobox protein homolog 1	CBX1	21,4	4,93	hoch
124	Q14839	Chromodomain-helicase-DNA-binding protein 4	CHD4	217,9	5,86	1,66
125	P53675	Clathrin heavy chain 2	CLTCL1	186,9	5,85	0,66
126	Q14677	Clathrin interactor 1	CLINT1	68,2	6,42	0,54
127	O43809	Cleavage and polyadenylation specificity factor subunit 5	NUDT21	26,2	8,82	0,05
128	Q05048	Cleavage stimulation factor subunit 1	CSTF1	48,3	6,58	0,63
129	Q14019	Coactosin-like protein	COTL1	15,9	5,67	0,62
130	P23528	Cofilin-1	CFL1	18,5	8,09	0,61
131	Q16204	Coiled-coil domain-containing protein 6	CCDC6	53,3	7,34	runter

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132	Q14011	Cold-inducible RNA-binding protein	CIRBP	18,6	9,51	0,58
133	Q07021	Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	31,3	4,84	0,57
134	Q13363	C-terminal-binding protein 1	CTBP1	47,5	6,77	0,57
135	Q9UBG0	C-type mannose receptor 2	MRC2	166,6	5,83	runter
136	Q9H5V8	CUB domain-containing protein 1	CDCP1	92,9	7,96	hoch
137	Q13616	Cullin-1	CUL1	89,6	8,00	0,44
138	Q13618	Cullin-3	CUL3	88,9	8,48	0,38
139	P06493	Cyclin-dependent kinase 1	CDK1	34,1	8,40	0,65
140	Q00534	Cyclin-dependent kinase 6	CDK6	36,9	6,46	hoch
141	P04080	Cystatin-B	CSTB	11,1	7,56	0,49
142	Q16527	Cysteine and glycine-rich protein 2	CSRP2	20,9	8,62	0,29
143	P49589	Cysteine--tRNA ligase, cytoplasmic	CARS	85,4	6,76	0,59
144	P14854	Cytochrome c oxidase subunit 6B1	COX6B1	10,2	7,05	0,49
145	P21399	Cytoplasmic aconitate hydratase	ACO1	98,3	6,68	0,65
146	Q9Y5Y2	Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	28,8	5,83	runter
147	Q96KP4	Cytosolic non-specific dipeptidase	CNDP2	52,8	5,97	0,64
148	Q9H773	dCTP pyrophosphatase 1	DCTPP1	18,7	5,03	0,57
149	Q15392	Delta(24)-sterol reductase	DHCR24	60,1	8,16	0,66
150	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	ECH1	35,8	8,00	0,65
151	P54886	Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1	87,2	7,12	0,58
152	P49366	Deoxyhypusine synthase	DHPS	40,9	5,36	hoch
153	Q9Y3Z3	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	72,2	7,14	runter
154	P36957	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	DLST	48,7	8,95	0,23
155	Q86TI2	Dipeptidyl peptidase 9	DPP9	98,2	6,46	1,50
156	Q96PD2	Discoidin, CUB and LCCL domain-containing protein 2	DCBLD2	85,0	7,17	0,42
157	Q13443	Disintegrin and metalloproteinase domain-containing protein 9	ADAM9	90,5	7,52	0,41
158	Q12959	Disks large homolog 1	DLG1	100,4	5,76	runter
159	Q9NRW3	DNA dC->dU-editing enzyme APOBEC-3C	APOBEC3C	22,8	7,59	1,60
160	P43246	DNA mismatch repair protein Msh2	MSH2	104,7	5,77	0,44
161	Q92878	DNA repair protein RAD50	RAD50	153,8	6,89	4,67
162	P33991	DNA replication licensing factor MCM4	MCM4	96,5	6,74	0,47
163	P27695	DNA-(apurinic or apyrimidinic site) lyase	AX1	35,5	8,12	0,63
164	O15446	DNA-directed RNA polymerase I subunit RPA34	CD3EAP	55,0	8,51	runter
165	O75937	DnaJ homolog subfamily C member 8	DNAJC8	29,8	9,06	runter
166	O60762	Dolichol-phosphate mannosyltransferase subunit 1	DPM1	29,6	9,57	runter

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167	P46977	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	80,5	8,07	0,56
168	O95793	Double-stranded RNA-binding protein Staufen homolog 1	STAU1	63,1	9,44	0,60
169	Q9NUL3	Double-stranded RNA-binding protein Staufen homolog 2	STAU2	62,6	9,61	runter
170	Q9UJU6	Drebrin-like protein	DBNL	48,2	5,05	0,61
171	Q14203	Dynactin subunit 1	DCTN1	141,6	5,81	0,62
172	O00429	Dynamin-1-like protein	DNM1L	81,8	6,81	0,51
173	P50570	Dynamin-2	DNM2	98,0	7,44	0,59
174	Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1	HUWE1	481,6	5,22	0,51
175	Q63HN8	E3 ubiquitin-protein ligase RNF213	RNF213	591,0	6,48	0,41
176	O94874	E3 UFM1-protein ligase 1	UFL1	89,5	6,79	runter
177	Q9NZN4	EH domain-containing protein 2	EHD2	61,1	6,46	0,39
178	Q92616	eIF-2-alpha kinase activator GCN1	GCN1	292,6	7,47	0,33
179	P13804	Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	35,1	8,38	0,60
180	Q8IUD2	ELKS/Rab6-interacting/CAST family member 1	ERC1	128,0	5,97	runter
181	Q9NZ08	Endoplasmic reticulum aminopeptidase 1	ERAP1	107,2	6,46	0,38
182	P30040	Endoplasmic reticulum resident protein 29	ERP29	29,0	7,31	0,53
183	P42892	Endothelin-converting enzyme 1	ECE1	87,1	5,88	runter
184	P84090	Enhancer of rudimentary homolog	ERH	12,3	5,92	0,46
185	P42126	Enoyl-CoA delta isomerase 1, mitochondrial	ECI1	32,8	8,54	0,61
186	P30084	Enoyl-CoA hydratase, mitochondrial	ECHS1	31,4	8,07	0,65
187	P29317	Ephrin type-A receptor 2	EPHA2	108,2	6,23	1,99
188	P00533	Epidermal growth factor receptor	EGFR	134,2	6,68	0,55
189	Q9H6S3	Epidermal growth factor receptor kinase substrate 8-like protein 2	EPS8L2	80,6	6,84	0,45
190	Q8N766	ER membrane protein complex subunit 1	EMC1	111,7	7,66	2,11
191	O94905	Erlin-2	ERLIN2	37,8	5,62	hoch
192	Q96HE7	ERO1-like protein alpha	ERO1A	54,4	5,68	1,52
193	P27105	Erythrocyte band 7 integral membrane protein	STOM	31,7	7,88	2,29
194	P30042	ES1 protein homolog, mitochondrial	C21orf33	28,2	8,27	2,51
195	P38919	Eukaryotic initiation factor 4A-III	EIF4A3	46,8	6,73	0,49
196	P62495	Eukaryotic peptide chain release factor subunit 1	ETF1	49,0	5,71	1,57
197	P47813	Eukaryotic translation initiation factor 1A, X-chromosomal	EIF1AX	16,5	5,24	0,60
198	O14602	Eukaryotic translation initiation factor 1A, Y-chromosomal	EIF1AY	16,4	5,24	0,60
199	O75821	Eukaryotic translation initiation factor 3 subunit G	EIF3G	35,6	6,13	0,65
200	Q9UBQ5	Eukaryotic translation initiation factor 3 subunit K	EIF3K	25,0	4,93	2,27
201	P06730	Eukaryotic translation initiation factor 4E	EIF4E	25,1	6,15	0,16
202	Q15056	Eukaryotic translation initiation factor 4H	EIF4H	27,4	7,23	0,59

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203	P55010	Eukaryotic translation initiation factor 5	EIF5	49,2	5,58	0,56
204	P63241	Eukaryotic translation initiation factor 5A-1	EIF5A	16,8	5,24	0,59
205	Q6IS14	Eukaryotic translation initiation factor 5A-1-like	EIF5AL1	16,8	5,00	0,59
206	Q9GZV4	Eukaryotic translation initiation factor 5A-2	EIF5A2	16,8	5,58	0,59
207	Q9UIA9	Exportin-7	XPO7	123,8	6,32	runter
208	P15311	Ezrin	EZR	69,4	6,27	1,53
209	Q9Y5B9	FACT complex subunit SPT16	SUPT16H	119,8	5,66	0,61
210	P47755	F-actin-capping protein subunit alpha-2	CAPZA2	32,9	5,85	0,65
211	Q96AE4	Far upstream element-binding protein 1	FUBP1	67,5	7,61	0,62
212	Q92945	Far upstream element-binding protein 2	KHSRP	73,1	7,30	0,50
213	P14324	Farnesyl pyrophosphate synthase	FDPS	48,2	6,15	0,57
214	Q96CS3	FAS-associated factor 2	FAF2	52,6	5,62	1,53
215	Q01469	Fatty acid-binding protein, epidermal	FABP5	15,2	7,01	0,55
216	Q96AC1	Fermitin family homolog 2	FERMT2	77,8	6,70	0,58
217	P02751	Fibronectin	FN1	262,5	5,71	0,33
218	Q14315	Filamin-C	FLNC	290,8	5,97	1,58
219	P30043	Flavin reductase (NADPH)	BLVRB	22,1	7,65	0,52
220	O75955	Flotillin-1	FLOT1	47,3	7,49	0,32
221	Q13642	Four and a half LIM domains protein 1	FHL1	36,2	8,97	runter
222	Q14192	Four and a half LIM domains protein 2	FHL2	32,2	7,55	0,65
223	Q9NQ88	Fructose-2,6-bisphosphatase TIGAR	TIGAR	30,0	7,69	3,27
224	Q99999	Galactosylceramide sulfotransferase	GAL3ST1	48,7	8,62	0,49
225	P09382	Galectin-1	LGALS1	14,7	5,50	0,61
226	Q13630	GDP-L-fucose synthase	TSTA3	35,9	6,60	0,51
227	P78347	General transcription factor II-I	GTF2I	112,3	6,39	0,29
228	O60763	General vesicular transport factor p115	USO1	107,8	4,91	0,61
229	P60983	Glia maturation factor beta	GMFB	16,7	5,29	0,32
230	P46926	Glucosamine-6-phosphate isomerase 1	GNPDA1	32,6	6,92	runter
231	P14314	Glucosidase 2 subunit beta	PRKCSH	59,4	4,41	3,00
232	O94925	Glutaminase kidney isoform, mitochondrial	GLS	73,4	7,77	0,61
233	P47897	Glutamine--tRNA ligase	QARS	87,7	7,15	0,55
234	P48637	Glutathione synthetase	GSS	52,4	5,92	0,37
235	P41250	Glycine--tRNA ligase	GARS	83,1	7,03	0,47
236	P11217	Glycogen phosphorylase, muscle form	PYGM	97,0	7,03	runter
237	Q9HC38	Glyoxalase domain-containing protein 4	GLOD4	34,8	5,60	0,49
238	Q9H4A6	Golgi phosphoprotein 3	GOLPH3	33,8	6,44	0,29
239	Q9H8Y8	Golgi reassembly-stacking protein 2	GORASP2	47,1	4,82	0,47

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs.* siNNMT
240	Q9H3P7	Golgi resident protein GCP60	ACBD3	60,6	5,06	0,59
241	Q08378	Golgin subfamily A member 3	GOLGA3	167,3	5,44	runter
242	Q99988	Growth/differentiation factor 15	GDF15	34,1	9,66	hoch
243	P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	GNB1	37,4	6,00	0,55
244	P32455	Guanylate-binding protein 1	GBP1	67,9	6,32	0,40
245	Q9Y450	HBS1-like protein	HBS1L	75,4	6,61	runter
246	O43301	Heat shock 70 kDa protein 12A	HSPA12A	74,9	6,77	runter
247	P0DMV9	Heat shock 70 kDa protein 1B	HSPA1B	70,0	5,66	2,80
248	P34931	Heat shock 70 kDa protein 1-like	HSPA1L	70,3	6,02	2,40
249	Q92598	Heat shock protein 105 kDa	HSPH1	96,8	5,39	1,63
250	Q9NRV9	Heme-binding protein 1	HEBP1	21,1	5,80	0,18
251	P08581	Hepatocyte growth factor receptor	MET	155,4	7,33	runter
252	Q7Z4V5	Hepatoma-derived growth factor-related protein 2	HDGFRP2	74,3	7,49	runter
253	Q14103	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	38,4	7,81	0,64
254	P55795	Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	49,2	6,30	0,32
255	O15347	High mobility group protein B3	HMGB3	23,0	8,37	runter
256	P52926	High mobility group protein HMGI-C	HMGA2	11,8	10,62	runter
257	P49773	Histidine triad nucleotide-binding protein 1	HINT1	13,8	6,95	runter
258	Q92522	Histone H1x	H1FX	22,5	10,76	hoch
259	Q96QV6	Histone H2A type 1-A	HIST1H2AA	14,2	10,86	0,47
260	P16104	Histone H2AX	H2AFX	15,1	10,74	0,47
261	P62805	Histone H4	HIST1H4A	11,4	11,36	0,55
262	Q86X55	Histone-arginine methyltransferase CARM1	CARM1	65,8	6,73	runter
263	P04439	HLA class I histocompatibility antigen, A-3 alpha chain	HLA-A	40,8	6,00	0,66
264	P51610	Host cell factor 1	HCFC1	208,6	7,46	0,58
265	Q9NX55	Huntingtin-interacting protein K	HYPK	14,7	4,93	runter
266	Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HADH	34,3	8,85	1,65
267	Q01581	Hydroxymethylglutaryl-CoA synthase, cytoplasmic	HMGCS1	57,3	5,41	0,39
268	Q70UQ0	Inhibitor of nuclear factor kappa-B kinase-interacting protein	IKBIP	39,3	9,17	0,59
269	Q9H2U2	Inorganic pyrophosphatase 2, mitochondrial	PPA2	37,9	7,39	0,65
270	P12268	Inosine-5'-monophosphate dehydrogenase 2	IMPDH2	55,8	6,90	0,64
271	O00425	Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	63,7	8,87	0,47
272	Q16270	Insulin-like growth factor-binding protein 7	IGFBP7	29,1	7,90	0,44
273	P26006	Integrin alpha-3	ITGA3	116,5	6,77	0,39
274	P06756	Integrin alpha-V	ITGAV	116,0	5,68	0,40
275	P05556	Integrin beta-1	ITGB1	88,4	5,39	0,60
276	Q13418	Integrin-linked protein kinase	ILK	51,4	8,07	0,55

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs.* siNNMT
277	P05362	Intercellular adhesion molecule 1	ICAM1	57,8	7,99	1,95
278	P19525	Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	62,1	8,40	0,48
279	Q27J81	Inverted formin-2	INF2	135,5	5,38	0,52
280	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic	IDH1	46,6	7,01	0,37
281	Q13907	Isopentenyl-diphosphate Delta-isomerase 1	IDI1	26,3	6,34	0,57
282	O94819	Kelch repeat and BTB domain-containing protein 11	KBTBD11	65,7	6,07	runter
283	Q07866	Kinesin light chain 1	KLC1	65,3	6,20	0,66
284	Q14739	Lamin-B receptor	LBR	70,7	9,36	2,49
285	Q9NRN7	L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	AASDHPPT	35,8	6,80	2,33
286	O95202	LETM1 and EF-hand domain-containing protein 1, mitochondrial	LETM1	83,3	6,70	runter
287	Q9NQ48	Leucine zipper transcription factor-like protein 1	LZTFL1	34,6	5,36	runter
288	Q32MZ4	Leucine-rich repeat flightless-interacting protein 1	LRRFIP1	89,2	4,65	0,59
289	P30740	Leukocyte elastase inhibitor	SERPINB1	42,7	6,28	0,53
290	P09960	Leukotriene A-4 hydrolase	LTA4H	69,2	6,18	0,51
291	O60488	Long-chain-fatty-acid--CoA ligase 4	ACSL4	79,1	8,38	0,17
292	P10619	Lysosomal protective protein	CTSA	54,4	6,61	0,63
293	P40925	Malate dehydrogenase, cytoplasmic	MDH1	36,4	7,36	0,52
294	Q13724	Mannosyl-oligosaccharide glucosidase	MOGS	91,9	8,90	2,10
295	P49006	MARCKS-related protein	MARCKSL1	19,5	4,67	0,62
296	Q14676	Mediator of DNA damage checkpoint protein 1	MDC1	226,5	5,47	4,60
297	Q9UNF1	Melanoma-associated antigen D2	MAGED2	64,9	9,32	0,27
298	O15173	Membrane-associated progesterone receptor component 2	PGRMC2	23,8	4,88	0,58
299	P53582	Methionine aminopeptidase 1	METAP1	43,2	7,17	0,55
300	Q16891	MIC complex subunit MIC60	IMMT	83,6	6,48	0,66
301	P27816	Microtubule-associated protein 4	MAP4	120,9	5,43	0,60
302	Q9UPY8	Microtubule-associated protein RP/EB family member 3	MAPRE3	32,0	5,54	runter
303	Q7Z434	Mitochondrial antiviral-signaling protein	MAVS	56,5	5,52	runter
304	O43615	Mitochondrial import inner membrane translocase subunit TIM44	TIMM44	51,3	8,32	0,59
305	O96008	Mitochondrial import receptor subunit TOM40 homolog	TOMM40	37,9	7,25	0,60
306	Q8IXI1	Mitochondrial Rho GTPase 2	RHOT2	68,1	5,86	runter
307	Q16539	Mitogen-activated protein kinase 14	MAPK14	41,3	5,78	runter
308	Q96T76	MMS19 nucleotide excision repair protein homolog	MMS19	113,2	6,35	0,33
309	Q9Y3A3	MOB-like protein phocein	MOB4	26,0	5,78	runter
310	P53985	Monocarboxylate transporter 1	SLC16A1	53,9	8,66	hoch
311	Q99685	Monoglyceride lipase	MGLL	33,2	6,99	0,64

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312	P84022	Mothers against decapentaplegic homolog 3	SMAD3	48,1	7,15	0,53
313	Q9NUJ1	Mycophenolic acid acyl-glucuronide esterase, mitochondrial	ABHD10	33,9	8,57	0,66
314	P35579	Myosin-9	MYH9	226,4	5,60	0,60
315	O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	DDAH1	31,1	5,81	runter
316	O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	SLC9A3R1	38,8	5,77	0,61
317	Q86SF2	N-acetylgalactosaminyltransferase 7	GALNT7	75,3	7,11	runter
318	P15559	NAD(P)H dehydrogenase [quinone] 1	NQO1	30,8	8,88	0,51
319	Q8NCW5	NAD(P)H-hydrate epimerase	NAXE	31,7	7,66	0,46
320	Q9NXA8	NAD-dependent protein deacylase sirtuin-5, mitochondrial	SIRT5	33,9	8,47	runter
321	O95299	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	40,7	8,48	runter
322	O75251	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	23,5	9,99	runter
323	P28331	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	79,4	6,23	4,11
324	P48163	NADP-dependent malic enzyme	ME1	64,1	6,13	0,56
325	Q8TBC4	NEDD8-activating enzyme E1 catalytic subunit	UBA3	51,8	5,45	1,92
326	Q15758	Neutral amino acid transporter B(0)	SLC1A5	56,6	5,48	2,28
327	Q6PIU2	Neutral cholesterol ester hydrolase 1	NCEH1	45,8	7,23	1,58
328	Q969V3	Nicalin	NCLN	62,9	6,89	0,54
329	**P40261**	**Nicotinamide N-methyltransferase**	**NNMT**	**29,6**	**5,74**	**0,09**
330	P22307	Non-specific lipid-transfer protein	SCP2	59,0	6,89	runter
331	Q9Y266	Nuclear migration protein nudC	NUDC	38,2	5,38	1,62
332	P57740	Nuclear pore complex protein Nup107	NUP107	106,3	5,43	0,18
333	P49790	Nuclear pore complex protein Nup153	NUP153	153,8	8,73	runter
334	Q92621	Nuclear pore complex protein Nup205	NUP205	227,8	6,19	1,66
335	Q9UKX7	Nuclear pore complex protein Nup50	NUP50	50,1	7,06	runter
336	P52948	Nuclear pore complex protein Nup98-Nup96	NUP98	197,5	6,40	0,35
337	P37198	Nuclear pore glycoprotein p62	NUP62	53,2	5,31	0,41
338	Q86WB0	Nuclear-interacting partner of ALK	ZC3HC1	55,2	5,62	runter
339	Q14978	Nucleolar and coiled-body phosphoprotein 1	NOLC1	73,6	9,47	1,73
340	Q9NR30	Nucleolar RNA helicase 2	DDX21	87,3	9,28	2,14
341	P17480	Nucleolar transcription factor 1	UBTF	89,4	5,81	runter
342	P19338	Nucleolin	NCL	76,6	4,70	1,50
343	Q96EE3	Nucleoporin SEH1	SEH1L	39,6	8,09	0,61
344	P12270	Nucleoprotein TPR	TPR	267,1	5,02	0,55
345	P22392	Nucleoside diphosphate kinase B	NME2	17,3	8,41	1,81
346	Q8WVJ2	NudC domain-containing protein 2	NUDCD2	17,7	5,07	0,55

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs.* siNNMT
347	Q9NX40	OCIA domain-containing protein 1	OCIAD1	27,6	7,49	0,65
348	Q56VL3	OCIA domain-containing protein 2	OCIAD2	16,9	9,03	0,64
349	P04181	Ornithine aminotransferase, mitochondrial	OAT	48,5	7,03	0,31
350	P10451	Osteopontin	SPP1	35,4	4,58	runter
351	P22059	Oxysterol-binding protein 1	OSBP	89,4	7,30	runter
352	Q9BZF1	Oxysterol-binding protein-related protein 8	OSBPL8	101,1	6,96	1,83
353	Q8WX93	Palladin	PALLD	150,5	7,09	4,64
354	O75475	PC4 and SFRS1-interacting protein	PSIP1	60,1	9,13	runter
355	O00151	PDZ and LIM domain protein 1	PDLIM1	36,0	7,02	0,59
356	Q96HC4	PDZ and LIM domain protein 5	PDLIM5	63,9	8,21	0,47
357	P62937	Peptidyl-prolyl cis-trans isomerase A	PPIA	18,0	7,81	0,66
358	P30405	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	PPIF	22,0	9,38	0,49
359	Q96AY3	Peptidyl-prolyl cis-trans isomerase FKBP10	FKBP10	64,2	5,62	0,36
360	P26885	Peptidyl-prolyl cis-trans isomerase FKBP2	FKBP2	15,6	9,13	runter
361	Q9H2H8	Peptidyl-prolyl cis-trans isomerase-like 3	PPIL3	18,1	6,79	1,99
362	Q8WW12	PEST proteolytic signal-containing nuclear protein	PCNP	18,9	7,49	0,55
363	Q8IWS0	PHD finger protein 6	PHF6	41,3	8,68	0,25
364	Q13492	Phosphatidylinositol-binding clathrin assembly protein	PICALM	70,7	7,90	0,56
365	O95394	Phosphoacetylglucosamine mutase	PGM3	59,8	6,25	runter
366	P36871	Phosphoglucomutase-1	PGM1	61,4	6,76	0,46
367	Q9GZP4	PITH domain-containing protein 1	PITHD1	24,2	5,74	2,69
368	P23634	Plasma membrane calcium-transporting ATPase 4	ATP2B4	137,8	6,60	hoch
369	P13796	Plastin-2	LCP1	70,2	5,43	1,91
370	Q15149	Plectin	PLEC	531,5	5,96	0,41
371	O43660	Pleiotropic regulator 1	PLRG1	57,2	9,17	runter
372	P09874	Poly [ADP-ribose] polymerase 1	PARP1	113,0	8,88	0,44
373	Q15365	Poly(rC)-binding protein 1	PCBP1	37,5	7,09	0,56
374	Q86U42	Polyadenylate-binding protein 2	PABPN1	32,7	5,06	0,54
375	Q9H074	Polyadenylate-binding protein-interacting protein 1	PAIP1	53,5	4,81	2,04
376	O95758	Polypyrimidine tract-binding protein 3	PTBP3	59,7	9,04	runter
377	Q9UHV9	Prefoldin subunit 2	PFDN2	16,6	6,58	runter
378	Q6UN15	Pre-mRNA 3'-end-processing factor FIP1	FIP1L1	66,5	5,59	runter
379	P46087	Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase	NOP2	89,2	9,23	2,06
380	Q8NDH3	Probable aminopeptidase NPEPL1	NPL1	55,8	6,87	runter
381	Q92841	Probable ATP-dependent RNA helicase DDX17	DDX17	80,2	8,27	0,62
382	Q7L014	Probable ATP-dependent RNA helicase DDX46	DDX46	117,3	9,29	runter
383	Q5GLZ8	Probable E3 ubiquitin-protein ligase HERC4	HERC4	118,5	6,19	0,54

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs.* siNNMT
384	Q99848	Probable rRNA-processing protein EBP2	EBNA1BP2	34,8	10,10	hoch
385	P07737	Profilin-1	PFN1	15,0	8,27	0,47
386	Q53EL6	Programmed cell death protein 4	PDCD4	51,7	5,21	runter
387	P35232	Prohibitin	PHB	29,8	5,76	0,57
388	O15460	Prolyl 4-hydroxylase subunit alpha-2	P4HA2	60,9	5,71	0,47
389	P07602	Prosaposin	PSAP	58,1	5,17	0,50
390	Q14914	Prostaglandin reductase 1	PTGR1	35,8	8,29	2,11
391	Q06323	Proteasome activator complex subunit 1	PSME1	28,7	6,02	0,48
392	Q9UL46	Proteasome activator complex subunit 2	PSME2	27,4	5,73	0,66
393	P28070	Proteasome subunit beta type-4	PSMB4	29,2	5,97	0,53
394	Q5VYK3	Proteasome-associated protein ECM29 homolog	ECM29	204,2	7,12	0,47
395	Q8IVF2	Protein AHNAK2	AHNAK2	616,2	5,36	hoch
396	Q9H694	Protein bicaudal C homolog 1	BICC1	104,8	8,54	0,37
397	Q9UKY7	Protein CDV3 homolog	CDV3	27,3	6,40	0,49
398	O00622	Protein CYR61	CYR61	42,0	8,21	1,51
399	P49257	Protein ERGIC-53	LMAN1	57,5	6,77	0,47
400	Q96C01	Protein FAM136A	FAM136A	15,6	7,61	0,63
401	Q52LJ0	Protein FAM98B	FAM98B	37,2	6,29	0,64
402	Q9UNF0	Protein kinase C and casein kinase substrate in neurons protein 2	PACSIN2	55,7	5,20	0,56
403	Q86UE4	Protein LYRIC	MTDH	63,8	9,32	2,04
404	Q9UFN0	Protein NipSnap homolog 3A	NIPSNAP3A	28,4	9,16	runter
405	Q9BUH6	Protein PAXX	C9orf142	21,6	5,48	runter
406	Q9BVG4	Protein PBDC1	PBDC1	26,0	4,79	runter
407	P41236	Protein phosphatase inhibitor 2	PPP1R2	23,0	4,74	0,64
408	Q6NXS1	Protein phosphatase inhibitor 2-like protein 3	PPP1R2P3	23,0	4,92	0,64
409	P29590	Protein PML	PML	97,5	6,21	0,61
410	P55735	Protein SEC13 homolog	SEC13	35,5	5,48	0,57
411	Q92734	Protein TFG	TFG	43,4	5,10	0,31
412	Q15436	Protein transport protein Sec23A	SEC23A	86,1	7,08	0,56
413	Q15437	Protein transport protein Sec23B	SEC23B	86,4	6,89	hoch
414	P53992	Protein transport protein Sec24C	SEC24C	118,2	7,06	0,55
415	O94855	Protein transport protein Sec24D	SEC24D	112,9	7,25	0,56
416	O94979	Protein transport protein Sec31A	SEC31A	132,9	6,89	0,20
417	Q9H993	Protein-glutamate O-methyltransferase	ARMT1	51,1	5,76	runter
418	A6NEC2	Puromycin-sensitive aminopeptidase-like protein	NPPSL1	53,7	5,34	0,63
419	Q9HCE1	Putative helicase MOV-10	MOV10	113,6	8,82	runter
420	O60361	Putative nucleoside diphosphate kinase	NME2P1	15,5	8,57	1,96

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421	Q9NQ29	Putative RNA-binding protein Luc7-like 1	LUC7L	43,7	9,92	runter
422	Q6P996	Pyridoxal-dependent decarboxylase domain-containing protein 1	PDXDC1	86,7	5,38	0,54
423	Q9NVS9	Pyridoxine-5'-phosphate oxidase	PNPO	30,0	7,06	runter
424	P08559	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	43,3	8,06	1,57
425	O00330	Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	54,1	8,66	hoch
426	P52306	Rap1 GTPase-GDP dissociation stimulator 1	RAP1GDS1	66,3	5,31	1,60
427	Q13283	Ras GTPase-activating protein-binding protein 1	G3BP1	52,1	5,52	0,64
428	Q9NP72	Ras-related protein Rab-18	RAB18	23,0	5,24	0,64
429	P61019	Ras-related protein Rab-2A	RAB2A	23,5	6,54	0,48
430	Q15286	Ras-related protein Rab-35	RAB35	23,0	8,29	4,00
431	P11233	Ras-related protein Ral-A	RALA	23,6	7,11	0,46
432	P11234	Ras-related protein Ral-B	RALB	23,4	6,62	runter
433	P61224	Ras-related protein Rap-1b	RAP1B	20,8	5,78	0,54
434	A6NIZ1	Ras-related protein Rap-1b-like protein	2 SV	20,9	5,48	0,54
435	P18754	Regulator of chromosome condensation	RCC1	44,9	7,52	0,66
436	P35249	Replication factor C subunit 4	RFC4	39,7	8,02	hoch
437	P27694	Replication protein A 70 kDa DNA-binding subunit	RPA1	68,1	7,21	0,53
438	Q14257	Reticulocalbin-2	RCN2	36,9	4,40	hoch
439	Q9NQC3	Reticulon-4	RTN4	129,9	4,50	0,51
440	P00352	Retinal dehydrogenase 1	ALDH1A1	54,8	6,73	0,31
441	P52565	Rho GDP-dissociation inhibitor 1	ARHGDIA	23,2	5,11	0,66
442	Q07960	Rho GTPase-activating protein 1	ARHGAP1	50,4	6,29	0,40
443	Q8N392	Rho GTPase-activating protein 18	ARHGAP18	74,9	6,44	0,60
444	P31350	Ribonucleoside-diphosphate reductase subunit M2	RRM2	44,8	5,38	1,61
445	Q7LG56	Ribonucleoside-diphosphate reductase subunit M2 B	RRM2B	40,7	4,97	1,80
446	P11908	Ribose-phosphate pyrophosphokinase 2	PRPS2	34,7	6,61	runter
447	Q15418	Ribosomal protein S6 kinase alpha-1	RPS6KA1	82,7	7,83	0,35
448	P51812	Ribosomal protein S6 kinase alpha-3	RPS6KA3	83,7	6,89	0,46
449	Q14137	Ribosome biogenesis protein BOP1	BOP1	83,6	6,19	2,10
450	Q9Y3A5	Ribosome maturation protein SBDS	SBDS	28,7	8,75	1,98
451	Q14498	RNA-binding protein 39	RBM39	59,3	10,10	1,55
452	Q9BWF3	RNA-binding protein 4	RBM4	40,3	7,08	1,71
453	Q01844	RNA-binding protein EWS	EWSR1	68,4	9,33	0,59
454	P22087	rRNA 2'-O-methyltransferase fibrillarin	FBL	33,8	10,18	0,59
455	Q5JTH9	RRP12-like protein	RRP12	143,6	8,75	2,44
456	Q8WVM8	Sec1 family domain-containing protein 1	SCFD1	72,3	6,27	runter

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457	Q15019	Septin-2	37500	41,5	6,60	0,63
458	P34896	Serine hydroxymethyltransferase, cytosolic	SHMT1	53,0	7,71	0,66
459	O75494	Serine/arginine-rich splicing factor 10	SRSF10	31,3	11,27	0,52
460	Q13247	Serine/arginine-rich splicing factor 6	SRSF6	39,6	11,43	4,38
461	Q16629	Serine/arginine-rich splicing factor 7	SRSF7	27,4	11,82	runter
462	Q13242	Serine/arginine-rich splicing factor 9	SRSF9	25,5	8,65	runter
463	Q9P289	Serine/threonine-protein kinase 26	STK26	46,5	5,29	0,31
464	O75914	Serine/threonine-protein kinase PAK 3	PAK3	62,3	5,45	hoch
465	Q14738	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	69,9	8,13	1,96
466	Q13362	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform	PPP2R5C	61,0	6,87	1,96
467	Q9BRF8	Serine/threonine-protein phosphatase CPPED1	CPD1	35,5	6,20	runter
468	P35237	Serpin B6	SERPINB6	42,6	5,27	0,45
469	Q96B97	SH3 domain-containing kinase-binding protein 1	SH3KBP1	73,1	6,62	runter
470	A0MZ66	Shootin-1	SHTN1	71,6	5,33	0,43
471	P08240	Signal recognition particle receptor subunit alpha	SRPRA	69,8	8,95	0,37
472	P42224	Signal transducer and activator of transcription 1-alpha/beta	STAT1	87,3	6,05	0,59
473	Q13126	S-methyl-5'-thioadenosine phosphorylase	MTAP	31,2	7,18	0,48
474	P05026	Sodium/potassium-transporting ATPase subunit beta-1	ATP1B1	35,0	8,53	runter
475	Q00796	Sorbitol dehydrogenase	SORD	38,3	7,97	2,28
476	P30626	Sorcin	SRI	21,7	5,59	0,47
477	Q13596	Sorting nexin-1	SNX1	59,0	5,15	runter
478	Q9Y5X1	Sorting nexin-9	SNX9	66,6	5,58	0,66
479	P19623	Spermidine synthase	SRM	33,8	5,49	0,58
480	Q13838	Spliceosome RNA helicase DDX39B	DDX39B	49,0	5,67	0,59
481	Q15637	Splicing factor 1	SF1	68,3	8,98	1,56
482	Q15459	Splicing factor 3A subunit 1	SF3A1	88,8	5,22	0,66
483	Q13435	Splicing factor 3B subunit 2	SF3B2	100,2	5,67	0,64
484	Q15393	Splicing factor 3B subunit 3	SF3B3	135,5	5,26	1,62
485	Q15427	Splicing factor 3B subunit 4	SF3B4	44,4	8,56	16,06
486	Q14247	Src substrate cortactin	CTTN	61,5	5,40	0,51
487	Q9H2G2	STE20-like serine/threonine-protein kinase	SLK	142,6	5,15	1,64
488	Q15738	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	NSDHL	41,9	8,06	0,53
489	Q14683	Structural maintenance of chromosomes protein 1A	SMC1A	143,1	7,64	runter
490	O95347	Structural maintenance of chromosomes protein 2	SMC2	135,6	8,43	runter
491	Q9UQE7	Structural maintenance of chromosomes protein 3	SMC3	141,5	7,18	0,65

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs.* siNNMT
492	Q96I99	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	46,5	6,39	0,51
493	Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial	SQRDL	49,9	9,11	0,49
494	O75940	Survival of motor neuron-related-splicing factor 30	SMNDC1	26,7	7,24	0,47
495	Q96A49	Synapse-associated protein 1	SYAP1	39,9	4,53	runter
496	Q8N3V7	Synaptopodin	SYNPO	99,4	8,72	0,66
497	Q15833	Syntaxin-binding protein 2	STXBP2	66,4	6,55	0,42
498	O00560	Syntenin-1	SDCBP	32,4	7,53	2,06
499	Q92804	TATA-binding protein-associated factor 2N	TAF15	61,8	8,02	0,42
500	P24821	Tenascin	TNC	240,7	4,89	2,79
501	Q9UGI8	Testin	TES	48,0	7,68	0,42
502	Q16881	Thioredoxin reductase 1, cytoplasmic	TXNRD1	70,9	7,39	0,65
503	O43396	Thioredoxin-like protein 1	TXNL1	32,2	4,96	1,54
504	Q9H3N1	Thioredoxin-related transmembrane protein 1	TMX1	31,8	4,98	0,41
505	P07996	Thrombospondin-1	THBS1	129,3	4,94	runter
506	P62328	Thymosin beta-4	TMSB4X	5,1	5,06	0,52
507	Q15654	Thyroid receptor-interacting protein 6	TRIP6	50,3	7,37	0,64
508	Q07157	Tight junction protein ZO-1	TJP1	195,3	6,70	0,61
509	Q9UDY2	Tight junction protein ZO-2	TJP2	133,9	7,40	1,90
510	P10646	Tissue factor pathway inhibitor	TFPI	35,0	8,25	hoch
511	P48307	Tissue factor pathway inhibitor 2	TFPI2	26,9	8,53	2,33
512	O14776	Transcription elongation regulator 1	TCERG1	123,8	8,65	runter
513	Q00059	Transcription factor A, mitochondrial	TFAM	29,1	9,72	0,27
514	P20290	Transcription factor BTF3	BTF3	22,2	9,38	runter
515	Q96K17	Transcription factor BTF3 homolog 4	BTF3L4	17,3	6,35	runter
516	Q04206	Transcription factor p65	RELA	60,2	5,68	runter
517	Q00577	Transcriptional activator protein Pur-alpha	PURA	34,9	6,44	hoch
518	P46937	Transcriptional coactivator YAP1	YAP1	54,4	5,17	0,31
519	Q12788	Transducin beta-like protein 3	TBL3	89,0	6,90	0,58
520	P02786	Transferrin receptor protein 1	TFRC	84,8	6,61	0,63
521	Q13595	Transformer-2 protein homolog alpha	TRA2A	32,7	11,27	hoch
522	P61586	Transforming protein RhoA	RHOA	21,8	6,10	0,66
523	Q15629	Translocating chain-associated membrane protein 1	TRAM1	43,0	9,63	0,66
524	P43307	Translocon-associated protein subunit alpha	SSR1	32,2	4,49	0,60
525	Q99805	Transmembrane 9 superfamily member 2	TM9SF2	75,7	7,44	hoch
526	Q92544	Transmembrane 9 superfamily member 4	TM9SF4	74,5	6,54	1,73
527	Q9Y3B3	Transmembrane emp24 domain-containing protein 7	TMED7	25,2	6,89	0,43
528	Q9Y5L0	Transportin-3	TNPO3	104,1	5,57	0,62

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs.* siNNMT
529	P40939	Trifunctional enzyme subunit alpha, mitochondrial	HADHA	82,9	9,04	0,65
530	P55084	Trifunctional enzyme subunit beta, mitochondrial	HADHB	51,3	9,41	0,64
531	P22102	Trifunctional purine biosynthetic protein adenosine-3	GART	107,7	6,70	0,54
532	P29144	Tripeptidyl-peptidase 2	TPP2	138,3	6,32	1,56
533	P23381	Tryptophan--tRNA ligase, cytoplasmic	WARS	53,1	6,23	0,63
534	P55327	Tumor protein D52	TPD52	24,3	4,83	0,39
535	Q6IBS0	Twinfilin-2	TWF2	39,5	6,84	0,27
536	P08621	U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70	51,5	9,94	0,47
537	Q53GS9	U4/U6.U5 tri-snRNP-associated protein 2	USP39	65,3	8,91	runter
538	Q96DI7	U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	39,3	8,10	runter
539	P45974	Ubiquitin carboxyl-terminal hydrolase 5	USP5	95,7	5,03	0,59
540	P09936	Ubiquitin carboxyl-terminal hydrolase isozyme L1	UCHL1	24,8	5,48	0,57
541	Q92890	Ubiquitin fusion degradation protein 1 homolog	UFD1L	34,5	6,70	2,22
542	Q14157	Ubiquitin-associated protein 2-like	UBAP2L	114,5	7,11	0,63
543	P68036	Ubiquitin-conjugating enzyme E2 L3	UBE2L3	17,9	8,51	0,55
544	Q13404	Ubiquitin-conjugating enzyme E2 variant 1	UBE2V1	16,5	7,93	2,25
545	P05161	Ubiquitin-like protein ISG15	ISG15	17,9	7,44	0,49
546	Q9NT62	Ubiquitin-like-conjugating enzyme ATG3	ATG3	35,8	4,74	hoch
547	Q14376	UDP-glucose 4-epimerase	GALE	38,3	6,73	0,63
548	O60701	UDP-glucose 6-dehydrogenase	UGDH	55,0	7,12	0,43
549	P19224	UDP-glucuronosyltransferase 1-6	UGT1A6	60,7	8,41	0,42
550	Q16222	UDP-N-acetylhexosamine pyrophosphorylase	UAP1	58,7	6,33	1,55
551	P30085	UMP-CMP kinase	CMPK1	22,2	5,57	0,52
552	Q9HB07	UPF0160 protein MYG1, mitochondrial	C12orf10	42,4	6,67	runter
553	Q9H3H3	UPF0696 protein C11orf68	C11orf68	27,3	5,45	hoch
554	Q03405	Urokinase plasminogen activator surface receptor	PLAUR	37,0	6,65	hoch
555	P46939	Utrophin	UTRN	394,2	5,33	0,45
556	O75351	Vacuolar protein sorting-associated protein 4B	VPS4B	49,3	7,23	hoch
557	Q9NP79	Vacuolar protein sorting-associated protein VTA1 homolog	VTA1	33,9	6,29	0,32
558	P50552	Vasodilator-stimulated phosphoprotein	VASP	39,8	8,94	2,01
559	P49748	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADVL	70,3	8,75	0,53
560	Q12907	Vesicular integral-membrane protein VIP36	LMAN2	40,2	6,95	0,48
561	P18206	Vinculin	VCL	123,7	5,66	0,66
562	Q9Y277	Voltage-dependent anion-selective channel protein 3	VDAC3	30,6	8,66	0,53
563	P38606	V-type proton ATPase catalytic subunit A	ATP6V1A	68,3	5,52	1,59
564	Q9UI12	V-type proton ATPase subunit H	ATP6V1H	55,8	6,48	1,97
565	Q8IWB7	WD repeat and FYVE domain-containing protein 1	WDFY1	46,3	7,33	3,25

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs.* siNNMT
566	Q9GZS3	WD repeat-containing protein 61	WDR61	33,6	5,47	runter
567	Q9Y6W5	Wiskott-Aldrich syndrome protein family member 2	WASF2	54,3	5,53	0,53
568	P16989	Y-box-binding protein 3	YBX3	40,1	9,77	0,54
569	Q8WU90	Zinc finger CCCH domain-containing protein 15	ZC3H15	48,6	5,31	runter
570	Q969S3	Zinc finger protein 622	ZNF622	54,2	6,15	hoch

Tabelle S8: Differenziell exprimierte Proteine von transient transfizierten 786-O Zellen bei 20 µM Methionin (sisc *vs*. siNNMT)

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs.* siNNMT
1	Q9C0C9	(E3-independent) E2 ubiquitin-conjugating enzyme	UBE2O	141,2	5,12	hoch
2	Q15029	116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	109,4	5,00	0,64
3	Q9C0C2	182 kDa tankyrase-1-binding protein	TNKS1BP1	181,7	4,86	0,65
4	Q6L8Q7	2',5'-phosphodiesterase 12	PDE12	67,3	6,57	hoch
5	Q9Y6K5	2'-5'-oligoadenylate synthase 3	OAS3	121,1	8,40	runter
6	P17980	26S protease regulatory subunit 6A	PSMC3	49,2	5,24	2,22
7	P43686	26S protease regulatory subunit 6B	PSMC4	47,3	5,21	1,52
8	O75832	26S proteasome non-ATPase regulatory subunit 10	PSMD10	24,4	6,10	hoch
9	Q9Y676	28S ribosomal protein S18b, mitochondrial	MRPS18B	29,4	9,38	0,62
10	P82675	28S ribosomal protein S5, mitochondrial	MRPS5	48,0	9,92	runter
11	O95861	3'(2'),5'-bisphosphate nucleotidase 1	BPNT1	33,4	5,69	runter
12	Q9BYD6	39S ribosomal protein L1, mitochondrial	MRPL1	36,9	8,78	1,77
13	Q96DV4	39S ribosomal protein L38, mitochondrial	MRPL38	44,6	7,53	0,31
14	Q13405	39S ribosomal protein L49, mitochondrial	MRPL49	19,2	9,45	hoch
15	P25398	40S ribosomal protein S12	RPS12	14,5	7,21	1,57
16	P62277	40S ribosomal protein S13	RPS13	17,2	10,54	0,34
17	P62263	40S ribosomal protein S14	RPS14	16,3	10,05	0,40
18	P62841	40S ribosomal protein S15	RPS15	17,0	10,39	0,56
19	P62244	40S ribosomal protein S15a	RPS15A	14,8	10,13	0,66
20	P62249	40S ribosomal protein S16	RPS16	16,4	10,21	0,55
21	P62269	40S ribosomal protein S18	RPS18	17,7	10,99	0,64
22	P21589	5'-nucleotidase	NT5E	63,3	7,03	1,96
23	P27635	60S ribosomal protein L10	RPL10	24,6	10,08	0,58
24	P61313	60S ribosomal protein L15	RPL15	24,1	11,62	0,58
25	Q07020	60S ribosomal protein L18	RPL18	21,6	11,72	0,59
26	Q02543	60S ribosomal protein L18a	RPL18A	20,7	10,71	1,50

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs.* siNNMT
27	P83731	60S ribosomal protein L24	RPL24	17,8	11,25	0,60
28	P61254	60S ribosomal protein L26	RPL26	17,2	10,55	0,30
29	Q9UNX3	60S ribosomal protein L26-like 1	RPL26L1	17,2	10,55	0,35
30	P46779	60S ribosomal protein L28	RPL28	15,7	12,02	0,60
31	P62888	60S ribosomal protein L30	RPL30	12,8	9,63	0,64
32	Q02878	60S ribosomal protein L6	RPL6	32,7	10,58	0,55
33	P18124	60S ribosomal protein L7	RPL7	29,2	10,65	0,47
34	P62424	60S ribosomal protein L7a	RPL7A	30,0	10,61	0,65
35	P62917	60S ribosomal protein L8	RPL8	28,0	11,03	0,63
36	Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic	ACAT2	41,3	6,92	1,84
37	O14561	Acyl carrier protein, mitochondrial	NDUFAB1	17,4	4,93	0,62
38	Q53H12	Acylglycerol kinase, mitochondrial	AGK	47,1	8,09	0,48
39	O43865	Adenosylhomocysteinase 2	AHCYL1	58,9	6,89	0,56
40	P54819	Adenylate kinase 2, mitochondrial	AK2	26,5	7,81	1,65
41	P00568	Adenylate kinase isoenzyme 1	AK1	21,6	8,63	2,08
42	Q8N6H7	ADP-ribosylation factor GTPase-activating protein 2	ARFGAP2	56,7	7,99	runter
43	P11766	Alcohol dehydrogenase class-3	ADH5	39,7	7,49	1,55
44	P05091	Aldehyde dehydrogenase, mitochondrial	ALDH2	56,3	7,05	0,44
45	P15121	Aldose reductase	AKR1B1	35,8	6,98	0,56
46	P30533	Alpha-2-macroglobulin receptor-associated protein	LRPAP1	41,4	8,78	2,40
47	P40222	Alpha-taxilin	TXLNA	61,9	6,52	1,69
48	Q7Z5R6	Amyloid beta A4 precursor protein-binding family B member 1-interacting protein	APBB1IP	73,1	5,59	1,60
49	Q06481	Amyloid-like protein 2	APLP2	86,9	4,79	0,33
50	O14617	AP-3 complex subunit delta-1	AP3D1	130,1	8,48	0,54
51	P24539	ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	28,9	9,36	0,31
52	Q5T2N8	ATPase family AAA domain-containing protein 3C	ATAD3C	46,4	9,31	1,55
53	P61221	ATP-binding cassette sub-family E member 1	ABCE1	67,3	8,34	0,65
54	P53396	ATP-citrate synthase	ACLY	120,8	7,33	1,75
55	P08237	ATP-dependent 6-phosphofructokinase, muscle type	PFKM	85,1	7,99	runter
56	Q9UMR2	ATP-dependent RNA helicase DDX19B	DDX19B	53,9	6,30	0,66
57	Q86XP3	ATP-dependent RNA helicase DDX42	DDX42	102,9	7,02	0,39
58	Q9Y6E2	Basic leucine zipper and W2 domain-containing protein 2	BZW2	48,1	6,68	0,63
59	P35613	Basigin	BSG	42,2	5,66	0,54
60	Q9NYF8	Bcl-2-associated transcription factor 1	BCLAF1	106,1	9,98	0,65
61	Q562R1	Beta-actin-like protein 2	ACTBL2	42,0	5,59	13,90
62	P13929	Beta-enolase	ENO3	47,0	7,71	1,79
63	P16278	Beta-galactosidase	GLB1	76,0	6,57	hoch

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs.* siNNMT
64	O95340	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2	PAPSS2	69,5	8,03	0,55
65	P80723	Brain acid soluble protein 1	BASP1	22,7	4,63	3,05
66	P27708	CAD protein	CAD	242,8	6,46	0,66
67	O75746	Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	74,7	8,38	runter
68	Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	74,1	8,62	0,52
69	Q9Y376	Calcium-binding protein 39	CAB39	39,8	6,89	0,48
70	Q05682	Caldesmon	CALD1	93,2	5,66	2,09
71	P07384	Calpain-1 catalytic subunit	CAPN1	81,8	5,67	0,51
72	O43852	Calumenin	CALU	37,1	4,64	2,01
73	O43570	Carbonic anhydrase 12	CA12	39,4	7,23	0,60
74	P00918	Carbonic anhydrase 2	CA2	29,2	7,40	0,28
75	Q14790	Caspase-8	CASP8	55,4	5,10	1,73
76	P07858	Cathepsin B	CTSB	37,8	6,30	3,03
77	P13987	CD59 glycoprotein	CD59	14,2	6,48	1,76
78	Q9H3Q1	Cdc42 effector protein 4	CDC42EP4	38,0	5,19	hoch
79	Q15642	Cdc42-interacting protein 4	TRIP10	68,3	5,73	1,51
80	Q96JB5	CDK5 regulatory subunit-associated protein 3	CDK5RAP3	56,9	4,75	0,58
81	Q9Y696	Chloride intracellular channel protein 4	CLIC4	28,8	5,59	0,44
82	P83916	Chromobox protein homolog 1	CBX1	21,4	4,93	hoch
83	Q14839	Chromodomain-helicase-DNA-binding protein 4	CHD4	217,9	5,86	1,57
84	P09496	Clathrin light chain A	CLTA	27,1	4,51	0,60
85	P09497	Clathrin light chain B	CLTB	25,2	4,64	5,83
86	Q96CT7	Coiled-coil domain-containing protein 124	CCDC124	25,8	9,54	1,55
87	Q07021	Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	31,3	4,84	0,62
88	Q9BT78	COP9 signalosome complex subunit 4	COPS4	46,2	5,83	1,80
89	P57737	Coronin-7	CORO7	100,5	5,80	0,51
90	Q9H5V8	CUB domain-containing protein 1	CDCP1	92,9	7,96	6,24
91	Q13617	Cullin-2	CUL2	86,9	6,92	runter
92	Q00534	Cyclin-dependent kinase 6	CDK6	36,9	6,46	hoch
93	Q00535	Cyclin-dependent-like kinase 5	CDK5	33,3	7,66	runter
94	Q9UHD1	Cysteine and histidine-rich domain-containing protein 1	CHORDC1	37,5	7,87	2,23
95	P49589	Cysteine--tRNA ligase, cytoplasmic	CARS	85,4	6,76	1,61
96	P14854	Cytochrome c oxidase subunit 6B1	COX6B1	10,2	7,05	1,66
97	P32321	Deoxycytidylate deaminase	DCTD	20,0	7,56	hoch
98	P49366	Deoxyhypusine synthase	DHPS	40,9	5,36	5,03

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs.* siNNMT
99	P33316	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial	DUT	26,5	9,36	1,86
100	P55039	Developmentally-regulated GTP-binding protein 2	DRG2	40,7	8,88	1,77
101	P27487	Dipeptidyl peptidase 4	DPP4	88,2	6,04	0,63
102	Q96PD2	Discoidin, CUB and LCCL domain-containing protein 2	DCBLD2	85,0	7,17	0,63
103	O00273	DNA fragmentation factor subunit alpha	DFFA	36,5	4,79	1,73
104	P52701	DNA mismatch repair protein Msh6	MSH6	152,7	6,90	0,46
105	Q92878	DNA repair protein RAD50	RAD50	153,8	6,89	runter
106	P11387	DNA topoisomerase 1	TOP1	90,7	9,31	1,86
107	P11388	DNA topoisomerase 2-alpha	TOP2A	174,3	8,72	0,66
108	O60884	DnaJ homolog subfamily A member 2	DNAJA2	45,7	6,48	1,51
109	Q9UBS4	DnaJ homolog subfamily B member 11	DNAJB11	40,5	6,18	2,18
110	Q8IXB1	DnaJ homolog subfamily C member 10	DNAJC10	91,0	7,18	2,38
111	Q99615	DnaJ homolog subfamily C member 7	DNAJC7	56,4	6,96	1,56
112	P46977	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	80,5	8,07	0,42
113	Q8TCJ2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	93,6	8,91	0,56
114	O95793	Double-stranded RNA-binding protein Staufen homolog 1	STAU1	63,1	9,44	0,39
115	P51452	Dual specificity protein phosphatase 3	DUSP3	20,5	7,80	hoch
116	Q14203	Dynactin subunit 1	DCTN1	141,6	5,81	0,54
117	Q9UJW0	Dynactin subunit 4	DCTN4	52,3	7,34	runter
118	Q9P0J7	E3 ubiquitin-protein ligase KCMF1	KCMF1	41,9	5,66	1,74
119	Q63HN8	E3 ubiquitin-protein ligase RNF213	RNF213	591,0	6,48	0,55
120	O94874	E3 UFM1-protein ligase 1	UFL1	89,5	6,79	runter
121	P43897	Elongation factor Ts, mitochondrial	TSFM	35,4	8,38	hoch
122	P42892	Endothelin-converting enzyme 1	ECE1	87,1	5,88	0,52
123	P84090	Enhancer of rudimentary homolog	ERH	12,3	5,92	1,91
124	O75521	Enoyl-CoA delta isomerase 2, mitochondrial	ECI2	43,6	9,00	1,95
125	P29317	Ephrin type-A receptor 2	EPHA2	108,2	6,23	1,65
126	P07099	Epoxide hydrolase 1	EPHX1	52,9	7,25	runter
127	Q8N766	ER membrane protein complex subunit 1	EMC1	111,7	7,66	2,34
128	O94905	Erlin-2	ERLIN2	37,8	5,62	hoch
129	Q96HE7	ERO1-like protein alpha	ERO1A	54,4	5,68	2,08
130	P30042	ES1 protein homolog, mitochondrial	C21orf33	28,2	8,27	2,97
131	P38919	Eukaryotic initiation factor 4A-III	EIF4A3	46,8	6,73	1,67
132	P23588	Eukaryotic translation initiation factor 4B	EIF4B	69,1	5,73	1,96
133	P63241	Eukaryotic translation initiation factor 5A-1	EIF5A	16,8	5,24	1,53

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs.* siNNMT
134	Q6IS14	Eukaryotic translation initiation factor 5A-1-like	EIF5AL1	16,8	5,00	2,16
135	Q9GZV4	Eukaryotic translation initiation factor 5A-2	EIF5A2	16,8	5,58	2,20
136	P55060	Exportin-2	CSE1L	110,3	5,77	0,61
137	Q9BSJ8	Extended synaptotagmin-1	ESYT1	122,8	5,83	0,60
138	A0FGR8	Extended synaptotagmin-2	ESYT2	102,3	9,26	2,04
139	Q9Y5B9	FACT complex subunit SPT16	SUPT16H	119,8	5,66	0,47
140	Q08945	FACT complex subunit SSRP1	SSRP1	81,0	6,87	0,47
141	Q96CS3	FAS-associated factor 2	FAF2	52,6	5,62	3,56
142	Q16658	Fascin	FSCN1	54,5	7,24	1,66
143	Q96AC1	Fermitin family homolog 2	FERMT2	77,8	6,70	0,22
144	P02751	Fibronectin	FN1	262,5	5,71	0,47
145	O75955	Flotillin-1	FLOT1	47,3	7,49	0,31
146	Q9NQ88	Fructose-2,6-bisphosphatase TIGAR	TIGAR	30,0	7,69	3,40
147	Q92820	Gamma-glutamyl hydrolase	GGH	35,9	7,11	0,62
148	O75223	Gamma-glutamylcyclotransferase	GGCT	21,0	5,14	1,88
149	Q13630	GDP-L-fucose synthase	TSTA3	35,9	6,60	0,65
150	P78347	General transcription factor II-I	GTF2I	112,3	6,39	0,61
151	Q8NBJ4	Golgi membrane protein 1	GOLM1	45,3	4,97	0,49
152	Q99988	Growth/differentiation factor 15	GDF15	34,1	9,66	hoch
153	Q9HAV7	GrpE protein homolog 1, mitochondrial	GRL1	24,3	8,12	1,67
154	Q9BVP2	Guanine nucleotide-binding protein-like 3	GNL3	62,0	9,16	2,78
155	Q9NX24	H/ACA ribonucleoprotein complex subunit 2	NHP2	17,2	8,22	1,95
156	O60832	H/ACA ribonucleoprotein complex subunit 4	DKC1	57,6	9,42	0,50
157	P0DMV9	Heat shock 70 kDa protein 1B	HSPA1B	70,0	5,66	1,55
158	O95757	Heat shock 70 kDa protein 4L	HSPA4L	94,5	5,88	1,69
159	Q92598	Heat shock protein 105 kDa	HSPH1	96,8	5,39	1,59
160	P04792	Heat shock protein beta-1	HSPB1	22,8	6,40	1,93
161	Q14568	Heat shock protein HSP 90-alpha A2	HSP90AA2P	39,3	4,65	0,51
162	P09601	Heme oxygenase 1	HMOX1	32,8	8,25	0,57
163	P30519	Heme oxygenase 2	HMOX2	36,0	5,41	2,10
164	Q9NRV9	Heme-binding protein 1	HEBP1	21,1	5,80	1,98
165	P08581	Hepatocyte growth factor receptor	MET	155,4	7,33	runter
166	P31943	Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	49,2	6,30	1,61
167	P26583	High mobility group protein B2	HMGB2	24,0	7,81	0,58
168	P37235	Hippocalcin-like protein 1	HPCAL1	22,3	5,35	1,62
169	Q02539	Histone H1.1	HIST1H1A	21,8	10,99	0,65
170	P16403	Histone H1.2	HIST1H1C	21,4	10,93	0,55

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs.* siNNMT
171	P16402	Histone H1.3	HIST1H1D	22,3	11,02	0,55
172	P10412	Histone H1.4	HIST1H1E	21,9	11,03	0,55
173	P16401	Histone H1.5	HIST1H1B	22,6	10,92	0,61
174	Q92522	Histone H1x	H1FX	22,5	10,76	2,00
175	P0C0S8	Histone H2A type 1	HIST1H2AG	14,1	10,90	0,62
176	P20671	Histone H2A type 1-D	HIST1H2AD	14,1	10,90	0,62
177	Q96KK5	Histone H2A type 1-H	HIST1H2AH	13,9	10,89	0,62
178	Q99878	Histone H2A type 1-J	HIST1H2AJ	13,9	10,89	0,62
179	Q6FI13	Histone H2A type 2-A	HIST2H2AA3	14,1	10,90	0,62
180	Q16777	Histone H2A type 2-C	HIST2H2AC	14,0	10,90	0,62
181	Q9BTM1	Histone H2A.J	H2AFJ	14,0	10,90	0,62
182	P62805	Histone H4	HIST1H4A	11,4	11,36	0,48
183	Q86X55	Histone-arginine methyltransferase CARM1	CARM1	65,8	6,73	runter
184	Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HADH	34,3	8,85	1,57
185	Q8TEX9	Importin-4	IPO4	118,6	4,96	runter
186	O95373	Importin-7	IPO7	119,4	4,82	0,58
187	P26006	Integrin alpha-3	ITGA3	116,5	6,77	0,43
188	P05106	Integrin beta-3	ITGB3	87,0	5,24	0,63
189	P05362	Intercellular adhesion molecule 1	ICAM1	57,8	7,99	2,23
190	P19525	Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	62,1	8,40	0,60
191	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic	IDH1	46,6	7,01	0,64
192	Q9NSE4	Isoleucine--tRNA ligase, mitochondrial	IARS2	113,7	7,20	2,12
193	Q96EK5	KIF1-binding protein	KIF1BP	71,8	5,49	1,80
194	Q14739	Lamin-B receptor	LBR	70,7	9,36	2,00
195	Q8NC56	LEM domain-containing protein 2	LEMD2	56,9	9,00	0,57
196	Q8N1G4	Leucine-rich repeat-containing protein 47	LRRC47	63,4	8,28	1,74
197	Q96AG4	Leucine-rich repeat-containing protein 59	LRRC59	34,9	9,57	0,63
198	Q9P2J5	Leucine--tRNA ligase, cytoplasmic	LARS	134,4	7,30	0,47
199	P05455	Lupus La protein	SSB	46,8	7,12	2,09
200	Q13724	Mannosyl-oligosaccharide glucosidase	MOGS	91,9	8,90	0,61
201	Q14676	Mediator of DNA damage checkpoint protein 1	MDC1	226,5	5,47	3,29
202	Q9UNF1	Melanoma-associated antigen D2	MAGED2	64,9	9,32	0,41
203	P55145	Mesencephalic astrocyte-derived neurotrophic factor	MANF	20,7	8,69	2,22
204	P50579	Methionine aminopeptidase 2	METAP2	52,9	5,82	1,62
205	O60220	Mitochondrial import inner membrane translocase subunit Tim8 A	TIMM8A	11,0	5,16	0,59
206	O75439	Mitochondrial-processing peptidase subunit beta	PMPCB	54,3	6,83	2,00

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207	Q96T76	MMS19 nucleotide excision repair protein homolog	MMS19	113,2	6,35	0,46
208	Q99685	Monoglyceride lipase	MGLL	33,2	6,99	0,65
209	Q9BQG0	Myb-binding protein 1A	MYBBP1A	148,8	9,28	0,63
210	O00499	Myc box-dependent-interacting protein 1	BIN1	64,7	5,06	1,74
211	P35580	Myosin-10	MYH10	228,9	5,54	0,52
212	O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	DDAH1	31,1	5,81	runter
213	Q86SF2	N-acetylgalactosaminyltransferase 7	GALNT7	75,3	7,11	runter
214	P15586	N-acetylglucosamine-6-sulfatase	GNS	62,0	8,31	2,35
215	P15559	NAD(P)H dehydrogenase [quinone] 1	NQO1	30,8	8,88	0,51
216	P48163	NADP-dependent malic enzyme	ME1	64,1	6,13	0,46
217	Q9UMX5	Neudesin	NENF	18,8	5,69	hoch
218	Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	628,7	6,15	1,56
219	Q15758	Neutral amino acid transporter B(0)	SLC1A5	56,6	5,48	1,81
220	Q6PIU2	Neutral cholesterol ester hydrolase 1	NCEH1	45,8	7,23	1,51
221	**P40261**	**Nicotinamide N-methyltransferase**	**NNMT**	**29,6**	**5,74**	**runter**
222	P43490	Nicotinamide phosphoribosyltransferase	NAMPT	55,5	7,15	1,83
223	Q15155	Nodal modulator 1	NOMO1	134,2	5,81	1,57
224	Q5JPE7	Nodal modulator 2	NOMO2	139,4	5,76	1,57
225	P69849	Nodal modulator 3	NOMO3	134,0	5,67	1,57
226	Q9Y266	Nuclear migration protein nudC	NUDC	38,2	5,38	1,58
227	P57740	Nuclear pore complex protein Nup107	NUP107	106,3	5,43	runter
228	Q99567	Nuclear pore complex protein Nup88	NUP88	83,5	5,69	0,59
229	P52948	Nuclear pore complex protein Nup98-Nup96	NUP98	197,5	6,40	runter
230	P37198	Nuclear pore glycoprotein p62	NUP62	53,2	5,31	2,13
231	Q02818	Nucleobindin-1	NUCB1	53,8	5,25	runter
232	Q9BZE4	Nucleolar GTP-binding protein 1	GTPBP4	73,9	9,50	0,55
233	Q7Z3B4	Nucleoporin p54	NUP54	55,4	7,02	2,16
234	P15531	Nucleoside diphosphate kinase A	NME1	17,1	6,19	1,72
235	Q96RS6	NudC domain-containing protein 1	NUDCD1	66,7	5,11	1,83
236	Q9Y3B8	Oligoribonuclease, mitochondrial	REXO2	26,8	6,87	hoch
237	P36551	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	CPOX	50,1	8,25	2,04
238	P22059	Oxysterol-binding protein 1	OSBP	89,4	7,30	0,62
239	Q9BZF1	Oxysterol-binding protein-related protein 8	OSBPL8	101,1	6,96	hoch
240	Q96HC4	PDZ and LIM domain protein 5	PDLIM5	63,9	8,21	0,52
241	O14908	PDZ domain-containing protein GIPC1	GIPC1	36,0	6,28	1,94
242	Q96EY7	Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	78,5	6,42	0,66

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243	P30405	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	PPIF	22,0	9,38	0,17
244	Q96AY3	Peptidyl-prolyl cis-trans isomerase FKBP10	FKBP10	64,2	5,62	0,55
245	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4	FKBP4	51,8	5,43	1,59
246	P30041	Peroxiredoxin-6	PRDX6	25,0	6,38	1,92
247	O00541	Pescadillo homolog	S1	68,0	7,33	0,57
248	Q8IWS0	PHD finger protein 6	PHF6	41,3	8,68	0,30
249	Q9Y285	Phenylalanine--tRNA ligase alpha subunit	FARSA	57,5	7,80	1,58
250	Q00325	Phosphate carrier protein, mitochondrial	SLC25A3	40,1	9,38	0,66
251	Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	70,7	7,62	0,47
252	Q96G03	Phosphoglucomutase-2	PGM2	68,2	6,73	2,13
253	O15067	Phosphoribosylformylglycinamidine synthase	PFAS	144,6	5,76	runter
254	Q9Y617	Phosphoserine aminotransferase	PSAT1	40,4	7,66	1,60
255	P20020	Plasma membrane calcium-transporting ATPase 1	ATP2B1	138,7	6,04	runter
256	P23634	Plasma membrane calcium-transporting ATPase 4	ATP2B4	137,8	6,60	2,49
257	Q14651	Plastin-1	PLS1	70,2	5,41	2,99
258	P13796	Plastin-2	LCP1	70,2	5,43	1,76
259	Q15149	Plectin	PLEC	531,5	5,96	0,65
260	P09874	Poly [ADP-ribose] polymerase 1	PARP1	113,0	8,88	0,52
261	Q9NX46	Poly(ADP-ribose) glycohydrolase ARH3	ADPRHL2	38,9	5,07	0,62
262	P57721	Poly(rC)-binding protein 3	PCBP3	39,4	8,07	1,94
263	Q13310	Polyadenylate-binding protein 4	PABPC4	70,7	9,26	runter
264	Q9H074	Polyadenylate-binding protein-interacting protein 1	PAIP1	53,5	4,81	1,51
265	Q10471	Polypeptide N-acetylgalactosaminyltransferase 2	GALNT2	64,7	8,35	0,66
266	O95758	Polypyrimidine tract-binding protein 3	PTBP3	59,7	9,04	runter
267	Q96AQ6	Pre-B-cell leukemia transcription factor-interacting protein 1	PBXIP1	80,6	5,33	runter
268	O94906	Pre-mRNA-processing factor 6	PRPF6	106,9	8,25	0,26
269	Q6P2Q9	Pre-mRNA-processing-splicing factor 8	PRPF8	273,4	8,84	0,58
270	Q96IZ0	PRKC apoptosis WT1 regulator protein	PAWR	36,5	5,41	1,68
271	P26196	Probable ATP-dependent RNA helicase DDX6	DDX6	54,4	8,66	0,54
272	O14737	Programmed cell death protein 5	PDCD5	14,3	6,04	1,58
273	Q99623	Prohibitin-2	PHB2	33,3	9,83	0,66
274	Q14914	Prostaglandin reductase 1	PTGR1	35,8	8,29	1,97
275	P49721	Proteasome subunit beta type-2	PSMB2	22,8	7,02	hoch
276	Q5VYK3	Proteasome-associated protein ECM29 homolog	ECM29	204,2	7,12	0,34
277	Q8IVF2	Protein AHNAK2	AHNAK2	616,2	5,36	0,63
278	Q9H694	Protein bicaudal C homolog 1	BICC1	104,8	8,54	0,55
279	P49257	Protein ERGIC-53	LMAN1	57,5	6,77	0,65

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280	Q92520	Protein FAM3C	FAM3C	24,7	8,29	1,92
281	Q86UE4	Protein LYRIC	MTDH	63,8	9,32	1,50
282	Q9Y316	Protein MEMO1	MEMO1	33,7	7,14	2,32
283	Q9UGV2	Protein NDRG3	NDRG3	41,4	5,31	0,47
284	Q9Y2Z0	Protein SGT1 homolog	SUGT1	41,0	5,16	3,13
285	Q92734	Protein TFG	TFG	43,4	5,10	0,40
286	O15027	Protein transport protein Sec16A	SEC16A	233,4	5,63	0,58
287	Q15437	Protein transport protein Sec23B	SEC23B	86,4	6,89	0,46
288	O94855	Protein transport protein Sec24D	SEC24D	112,9	7,25	0,37
289	O94979	Protein transport protein Sec31A	SEC31A	132,9	6,89	0,41
290	P00734	Prothrombin	F2	70,0	5,90	hoch
291	A6NGU5	Putative gamma-glutamyltranspeptidase 3	GGT3P	61,5	7,14	0,66
292	Q58FG0	Putative heat shock protein HSP 90-alpha A5	HSP90AA5P	38,7	6,57	0,18
293	Q6P996	Pyridoxal-dependent decarboxylase domain-containing protein 1	PDXDC1	86,7	5,38	0,65
294	Q9NVS9	Pyridoxine-5'-phosphate oxidase	PNPO	30,0	7,06	0,44
295	P11177	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	39,2	6,65	1,61
296	P52306	Rap1 GTPase-GDP dissociation stimulator 1	RAP1GDS1	66,3	5,31	2,47
297	P61026	Ras-related protein Rab-10	RAB10	22,5	8,38	0,65
298	P61019	Ras-related protein Rab-2A	RAB2A	23,5	6,54	0,51
299	Q8WUD1	Ras-related protein Rab-2B	RAB2B	24,2	7,83	0,49
300	Q15286	Ras-related protein Rab-35	RAB35	23,0	8,29	runter
301	P51148	Ras-related protein Rab-5C	RAB5C	23,5	8,41	0,62
302	Q9NQC3	Reticulon-4	RTN4	129,9	4,50	2,04
303	P00352	Retinal dehydrogenase 1	ALDH1A1	54,8	6,73	0,58
304	Q07960	Rho GTPase-activating protein 1	ARHGAP1	50,4	6,29	0,52
305	Q8N392	Rho GTPase-activating protein 18	ARHGAP18	74,9	6,44	0,54
306	Q92888	Rho guanine nucleotide exchange factor 1	ARHGEF1	102,4	5,66	1,78
307	P23921	Ribonucleoside-diphosphate reductase large subunit	RRM1	90,0	7,15	1,54
308	Q14137	Ribosome biogenesis protein BOP1	BOP1	83,6	6,19	0,36
309	Q8TDN6	Ribosome biogenesis protein BRX1 homolog	BRIX1	41,4	9,92	0,46
310	Q9GZL7	Ribosome biogenesis protein WDR12	WDR12	47,7	5,90	0,65
311	Q9Y3A5	Ribosome maturation protein SBDS	SBDS	28,7	8,75	1,82
312	Q9P2E9	Ribosome-binding protein 1	RRBP1	152,4	8,60	0,63
313	Q96E39	RNA binding motif protein, X-linked-like-1	RBMXL1	42,1	9,89	0,66
314	Q9H0A0	RNA cytidine acetyltransferase	NAT10	115,7	8,27	0,60
315	P38159	RNA-binding motif protein, X chromosome	RBMX	42,3	10,05	0,59

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316	P49756	RNA-binding protein 25	RBM25	100,1	6,32	runter
317	P98179	RNA-binding protein 3	RBM3	17,2	8,91	1,54
318	Q9BWF3	RNA-binding protein 4	RBM4	40,3	7,08	2,35
319	Q5JTH9	RRP12-like protein	RRP12	143,6	8,75	0,63
320	Q9Y230	RuvB-like 2	RUVBL2	51,1	5,64	1,62
321	Q8NBX0	Saccharopine dehydrogenase-like oxidoreductase	SCCPDH	47,1	9,14	runter
322	P82979	SAP domain-containing ribonucleoprotein	SARNP	23,7	6,42	1,57
323	Q9Y6Y8	SEC23-interacting protein	SEC23IP	111,0	5,54	1,54
324	P34896	Serine hydroxymethyltransferase, cytosolic	SHMT1	53,0	7,71	runter
325	O15269	Serine palmitoyltransferase 1	SPTLC1	52,7	6,01	0,33
326	Q13247	Serine/arginine-rich splicing factor 6	SRSF6	39,6	11,43	0,60
327	O75914	Serine/threonine-protein kinase PAK 3	PAK3	62,3	5,45	0,52
328	O95747	Serine/threonine-protein kinase R1	OXSR1	58,0	6,43	2,05
329	Q14738	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	69,9	8,13	runter
330	Q13362	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform	PPP2R5C	61,0	6,87	runter
331	Q5H9R7	Serine/threonine-protein phosphatase 6 regulatory subunit 3	PPP6R3	97,6	4,60	0,61
332	Q9BRF8	Serine/threonine-protein phosphatase CPPED1	CPD1	35,5	6,20	runter
333	P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	PPP1CA	37,5	6,33	0,18
334	P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	PPP1CB	37,2	6,19	2,12
335	P49591	Serine--tRNA ligase, cytoplasmic	SARS	58,7	6,43	2,15
336	A0MZ66	Shootin-1	SHTN1	71,6	5,33	0,44
337	P08240	Signal recognition particle receptor subunit alpha	SRPRA	69,8	8,95	0,21
338	P42224	Signal transducer and activator of transcription 1-alpha/beta	STAT1	87,3	6,05	0,65
339	Q13596	Sorting nexin-1	SNX1	59,0	5,15	runter
340	Q9NUQ6	SPATS2-like protein	SPATS2L	61,7	9,64	1,51
341	P19623	Spermidine synthase	SRM	33,8	5,49	0,49
342	Q15637	Splicing factor 1	SF1	68,3	8,98	1,89
343	Q15427	Splicing factor 3B subunit 4	SF3B4	44,4	8,56	3,37
344	Q01081	Splicing factor U2AF 35 kDa subunit	U2AF1	27,9	8,81	0,63
345	P26368	Splicing factor U2AF 65 kDa subunit	U2AF2	53,5	9,09	1,72
346	P38646	Stress-70 protein, mitochondrial	HSPA9	73,6	6,16	1,55
347	Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial	SQRDL	49,9	9,11	0,58
348	Q9UBE0	SUMO-activating enzyme subunit 1	SAE1	38,4	5,30	0,46
349	O75940	Survival of motor neuron-related-splicing factor 30	SMNDC1	26,7	7,24	1,72
350	O00161	Synaptosomal-associated protein 23	SNAP23	23,3	5,01	2,70

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351	O95721	Synaptosomal-associated protein 29	SNAP29	29,0	5,81	1,85
352	Q12846	Syntaxin-4	STX4	34,2	6,28	1,71
353	O15400	Syntaxin-7	STX7	29,8	5,55	0,57
354	P17987	T-complex protein 1 subunit alpha	TCP1	60,3	6,11	1,72
355	Q99614	Tetratricopeptide repeat protein 1	TTC1	33,5	4,84	1,55
356	O95881	Thioredoxin domain-containing protein 12	TXNDC12	19,2	5,40	1,50
357	Q9BRA2	Thioredoxin domain-containing protein 17	TXNDC17	13,9	5,52	1,79
358	Q8NBS9	Thioredoxin domain-containing protein 5	TXNDC5	47,6	5,97	1,78
359	P30048	Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	27,7	7,78	1,67
360	O43396	Thioredoxin-like protein 1	TXNL1	32,2	4,96	1,67
361	Q16762	Thiosulfate sulfurtransferase	TST	33,4	7,25	2,89
362	P07996	Thrombospondin-1	THBS1	129,3	4,94	runter
363	O75663	TIP41-like protein	TIPRL	31,4	5,91	2,42
364	P48307	Tissue factor pathway inhibitor 2	TFPI2	26,9	8,53	3,34
365	P20290	Transcription factor BTF3	BTF3	22,2	9,38	2,01
366	Q04206	Transcription factor p65	RELA	60,2	5,68	3,99
367	Q00577	Transcriptional activator protein Pur-alpha	PURA	34,9	6,44	2,02
368	P02786	Transferrin receptor protein 1	TFRC	84,8	6,61	0,63
369	P62995	Transformer-2 protein homolog beta	TRA2B	33,6	11,25	0,42
370	Q9Y6A5	Transforming acidic coiled-coil-containing protein 3	TACC3	90,3	5,05	hoch
371	P37802	Transgelin-2	TAGLN2	22,4	8,25	1,50
372	O43493	Trans-Golgi network integral membrane protein 2	TGOLN2	51,1	5,73	0,61
373	Q9NR50	Translation initiation factor eIF-2B subunit gamma	EIF2B3	50,2	6,47	hoch
374	P13693	Translationally-controlled tumor protein	TPT1	19,6	4,93	1,52
375	Q15629	Translocating chain-associated membrane protein 1	TRAM1	43,0	9,63	0,44
376	Q9HD45	Transmembrane 9 superfamily member 3	TM9SF3	67,8	7,21	0,66
377	Q9Y3B3	Transmembrane emp24 domain-containing protein 7	TMED7	25,2	6,89	runter
378	Q9Y5L0	Transportin-3	TNPO3	104,1	5,57	0,59
379	P60174	Triosephosphate isomerase	TPI1	30,8	5,92	1,55
380	P29144	Tripeptidyl-peptidase 2	TPP2	138,3	6,32	1,54
381	P07951	Tropomyosin beta chain	TPM2	32,8	4,70	1,53
382	Q71U36	Tubulin alpha-1A chain	TUBA1A	50,1	5,06	1,91
383	P23258	Tubulin gamma-1 chain	TUBG1	51,1	6,14	0,61
384	Q9NRH3	Tubulin gamma-2 chain	TUBG2	51,1	5,80	0,61
385	Q12792	Twinfilin-1	TWF1	40,3	6,96	1,78
386	Q6IBS0	Twinfilin-2	TWF2	39,5	6,84	0,54
387	Q05209	Tyrosine-protein phosphatase non-receptor type 12	PTPN12	88,1	5,62	2,27

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor sisc *vs.* siNNMT
388	P54577	Tyrosine--tRNA ligase, cytoplasmic	YARS	59,1	7,05	1,60
389	P09012	U1 small nuclear ribonucleoprotein A	SNRPA	31,3	9,83	0,62
390	O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	244,4	6,06	0,42
391	Q96DI7	U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	39,3	8,10	runter
392	Q14694	Ubiquitin carboxyl-terminal hydrolase 10	USP10	87,1	5,31	hoch
393	P45974	Ubiquitin carboxyl-terminal hydrolase 5	USP5	95,7	5,03	0,56
394	Q92890	Ubiquitin fusion degradation protein 1 homolog	UFD1L	34,5	6,70	2,13
395	Q15819	Ubiquitin-conjugating enzyme E2 variant 2	UBE2V2	16,4	8,09	hoch
396	P05161	Ubiquitin-like protein ISG15	ISG15	17,9	7,44	0,60
397	Q9NT62	Ubiquitin-like-conjugating enzyme ATG3	ATG3	35,8	4,74	1,54
398	P19224	UDP-glucuronosyltransferase 1-6	UGT1A6	60,7	8,41	runter
399	Q03405	Urokinase plasminogen activator surface receptor	PLAUR	37,0	6,65	hoch
400	Q96QK1	Vacuolar protein sorting-associated protein 35	VPS35	91,6	5,49	0,58
401	P50552	Vasodilator-stimulated phosphoprotein	VASP	39,8	8,94	1,51
402	O75396	Vesicle-trafficking protein SEC22b	SEC22B	24,6	6,92	0,63
403	P21283	V-type proton ATPase subunit C 1	ATP6V1C1	43,9	7,46	1,54
404	Q9UI12	V-type proton ATPase subunit H	ATP6V1H	55,8	6,48	1,54
405	Q969S3	Zinc finger protein 622	ZNF622	54,2	6,15	hoch
406	Q96KR1	Zinc finger RNA-binding protein	ZFR	116,9	9,04	0,66

Tabelle S9: Differenziell exprimierte Proteine von transient transfizierten 769-P Zellen bei 100 µM Methionin (mock *vs.* NNMT)

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
1	Q04446	1,4-alpha-glucan-branching enzyme	GBE1	80,4	6,32	runter
2	Q15029	116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	109,4	5,00	1,74
3	Q16698	2,4-dienoyl-CoA reductase, mitochondrial	DECR1	36,0	9,28	0,56
4	O75832	26S proteasome non-ATPase regulatory subunit 10	PSMD10	24,4	6,10	0,35
5	O00487	26S proteasome non-ATPase regulatory subunit 14	PSMD14	34,6	6,52	1,51
6	Q15008	26S proteasome non-ATPase regulatory subunit 6	PSMD6	45,5	5,62	1,70
7	P51665	26S proteasome non-ATPase regulatory subunit 7	PSMD7	37,0	6,77	1,99
8	Q9Y3D9	28S ribosomal protein S23, mitochondrial	MRPS23	21,8	8,90	hoch
9	P82675	28S ribosomal protein S5, mitochondrial	MRPS5	48,0	9,92	0,51
10	Q9ULD0	2-oxoglutarate dehydrogenase-like, mitochondrial	OGDHL	114,4	6,65	1,61
11	Q96DV4	39S ribosomal protein L38, mitochondrial	MRPL38	44,6	7,53	runter
12	Q9H9J2	39S ribosomal protein L44, mitochondrial	MRPL44	37,5	8,40	runter
13	P61247	40S ribosomal protein S3a	RPS3A	29,9	9,73	1,56

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
14	P22090	40S ribosomal protein S4, Y isoform 1	RPS4Y1	29,4	10,24	0,62
15	Q8TCD5	5'(3')-deoxyribonucleotidase, cytosolic type	NT5C	23,4	6,64	0,58
16	P61313	60S ribosomal protein L15	RPL15	24,1	11,62	1,52
17	Q02543	60S ribosomal protein L18a	RPL18A	20,7	10,71	1,56
18	P46779	60S ribosomal protein L28	RPL28	15,7	12,02	2,48
19	P39687	Acidic leucine-rich nuclear phosphoprotein 32 family member A	ANP32A	28,6	4,09	0,54
20	O14561	Acyl carrier protein, mitochondrial	NDUFAB1	17,4	4,93	3,89
21	Q53H12	Acylglycerol kinase, mitochondrial	AGK	47,1	8,09	0,65
22	P46108	Adapter molecule crk	CRK	33,8	5,55	0,61
23	P12235	ADP/ATP translocase 1	SLC25A4	33,0	9,76	hoch
24	P05141	ADP/ATP translocase 2	SLC25A5	32,8	9,69	hoch
25	P12236	ADP/ATP translocase 3	SLC25A6	32,8	9,74	hoch
26	Q9NRG9	Aladin	AAAS	59,5	7,50	2,48
27	Q9UHK6	Alpha-methylacyl-CoA racemase	AMACR	42,4	6,44	runter
28	Q13155	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	35,3	8,22	0,54
29	Q7Z5R6	Amyloid beta A4 precursor protein-binding family B member 1-interacting protein	APBB1IP	73,1	5,59	1,52
30	Q6FI81	Anamorsin	CIAPIN1	33,6	5,62	0,45
31	O75027	ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	82,6	9,33	hoch
32	Q8NE71	ATP-binding cassette sub-family F member 1	ABCF1	95,9	6,80	1,51
33	Q9NVP1	ATP-dependent RNA helicase DDX18	DDX18	75,4	9,50	1,99
34	O95816	BAG family molecular chaperone regulator 2	BAG2	23,8	6,70	0,56
35	Q7L1Q6	Basic leucine zipper and W2 domain-containing protein 1	BZW1	48,0	5,92	1,55
36	Q9Y6E2	Basic leucine zipper and W2 domain-containing protein 2	BZW2	48,1	6,68	2,40
37	P51572	B-cell receptor-associated protein 31	BCAP31	28,0	8,44	1,50
38	Q9NYF8	Bcl-2-associated transcription factor 1	BCLAF1	106,1	9,98	hoch
39	Q562R1	Beta-actin-like protein 2	ACTBL2	42,0	5,59	0,13
40	O95340	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2	PAPSS2	69,5	8,03	6,07
41	Q9UQB8	Brain-specific angiogenesis inhibitor 1-associated protein 2	BAIAP2	60,8	8,90	runter
42	Q9P287	BRCA2 and CDKN1A-interacting protein	BCCIP	36,0	4,61	hoch
43	Q9Y6D6	Brefeldin A-inhibited guanine nucleotide-exchange protein 1	ARFGEF1	208,6	5,85	10,89
44	O75844	CAAX prenyl protease 1 homolog	ZMPSTE24	54,8	7,49	0,64
45	O43852	Calumenin	CALU	37,1	4,64	1,63
46	P13861	cAMP-dependent protein kinase type II-alpha regulatory subunit	PRKAR2A	45,5	5,07	runter
47	P21964	Catechol O-methyltransferase	COMT	30,0	5,47	1,91

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
48	P11717	Cation-independent mannose-6-phosphate receptor	IGF2R	274,2	5,94	2,18
49	Q96JB5	CDK5 regulatory subunit-associated protein 3	CDK5RAP3	56,9	4,75	1,75
50	Q99459	Cell division cycle 5-like protein	CDC5L	92,2	8,18	runter
51	Q14839	Chromodomain-helicase-DNA-binding protein 4	CHD4	217,9	5,86	1,69
52	O43809	Cleavage and polyadenylation specificity factor subunit 5	NUDT21	26,2	8,82	0,38
53	Q12996	Cleavage stimulation factor subunit 3	CSTF3	82,9	8,12	0,64
54	Q14019	Coactosin-like protein	COTL1	15,9	5,67	0,62
55	Q9Y678	Coatomer subunit gamma-1	COPG1	97,7	5,47	1,85
56	Q96A33	Coiled-coil domain-containing protein 47	CCDC47	55,8	4,87	0,17
57	Q9NZB2	Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	121,8	8,88	1,77
58	P61201	COP9 signalosome complex subunit 2	COPS2	51,6	5,53	2,05
59	Q13617	Cullin-2	CUL2	86,9	6,92	hoch
60	P04080	Cystatin-B	CSTB	11,1	7,56	1,68
61	P07919	Cytochrome b-c1 complex subunit 6, mitochondrial	UQCRH	10,7	4,44	0,62
62	P99999	Cytochrome c	CYCS	11,7	9,57	1,76
63	P10606	Cytochrome c oxidase subunit 5B, mitochondrial	COX5B	13,7	8,81	0,57
64	Q9Y5Y2	Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	28,8	5,83	0,24
65	Q96GG9	DCN1-like protein 1	DCUN1D1	30,1	5,34	1,59
66	Q13443	Disintegrin and metalloproteinase domain-containing protein 9	ADAM9	90,5	7,52	0,65
67	Q9NRW3	DNA dC->dU-editing enzyme APOBEC-3C	APOBEC3C	22,8	7,59	hoch
68	P49736	DNA replication licensing factor MCM2	MCM2	101,8	5,52	1,71
69	O60762	Dolichol-phosphate mannosyltransferase subunit 1	DPM1	29,6	9,57	0,61
70	Q8TCJ2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	93,6	8,91	0,54
71	Q9UJW0	Dynactin subunit 4	DCTN4	52,3	7,34	hoch
72	Q9UII4	E3 ISG15--protein ligase HERC5	HERC5	116,8	7,65	hoch
73	Q5T4S7	E3 ubiquitin-protein ligase UBR4	UBR4	573,5	6,04	5,31
74	P42892	Endothelin-converting enzyme 1	ECE1	87,1	5,88	runter
75	P42566	Epidermal growth factor receptor substrate 15	EPS15	98,6	4,64	runter
76	O43324	Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1	19,8	8,54	1,84
77	O00303	Eukaryotic translation initiation factor 3 subunit F	EIF3F	37,5	5,45	6,86
78	O15372	Eukaryotic translation initiation factor 3 subunit H	EIF3H	39,9	6,54	0,35
79	Q9UBQ5	Eukaryotic translation initiation factor 3 subunit K	EIF3K	25,0	4,93	0,59
80	P23588	Eukaryotic translation initiation factor 4B	EIF4B	69,1	5,73	0,48
81	O60841	Eukaryotic translation initiation factor 5B	EIF5B	138,7	5,49	1,58
82	A0FGR8	Extended synaptotagmin-2	ESYT2	102,3	9,26	0,65
83	Q9Y5B9	FACT complex subunit SPT16	SUPT16H	119,8	5,66	1,55
84	Q9Y4F1	FERM, RhoGEF and pleckstrin domain-containing protein 1	FARP1	118,6	8,15	1,51

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
85	P02792	Ferritin light chain	FTL	20,0	5,78	0,46
86	Q53EP0	Fibronectin type III domain-containing protein 3B	FNDC3B	132,8	5,95	2,38
87	O75369	Filamin-B	FLNB	278,0	5,73	0,33
88	Q9NQ88	Fructose-2,6-bisphosphatase TIGAR	TIGAR	30,0	7,69	0,63
89	P16930	Fumarylacetoacetase	FAH	46,3	6,95	2,65
90	P19440	Gamma-glutamyltranspeptidase 1	GGT1	61,4	7,12	0,66
91	P57764	Gasdermin-D	GSDMD	52,8	5,08	1,77
92	P78347	General transcription factor II-I	GTF2I	112,3	6,39	1,72
93	Q9BQ67	Glutamate-rich WD repeat-containing protein 1	GRWD1	49,4	4,92	runter
94	P23378	Glycine dehydrogenase (decarboxylating), mitochondrial	GLDC	112,7	7,11	0,59
95	Q14C86	GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1	164,9	5,22	1,56
96	P63096	Guanine nucleotide-binding protein G(i) subunit alpha-1	GNAI1	40,3	5,97	0,55
97	O60832	H/ACA ribonucleoprotein complex subunit 4	DKC1	57,6	9,42	hoch
98	Q14568	Heat shock protein HSP 90-alpha A2	HSP90AA2P	39,3	4,65	1,53
99	Q9NRV9	Heme-binding protein 1	HEBP1	21,1	5,80	1,83
100	P08581	Hepatocyte growth factor receptor	MET	155,4	7,33	1,63
101	O14964	Hepatocyte growth factor-regulated tyrosine kinase substrate	HGS	86,1	6,16	0,45
102	P51858	Hepatoma-derived growth factor	HDGF	26,8	4,73	0,61
103	P09429	High mobility group protein B1	HMGB1	24,9	5,74	0,63
104	P26583	High mobility group protein B2	HMGB2	24,0	7,81	0,66
105	P52926	High mobility group protein HMGI-C	HMGA2	11,8	10,62	0,60
106	Q86X55	Histone-arginine methyltransferase CARM1	CARM1	65,8	6,73	0,52
107	Q16576	Histone-binding protein RBBP7	RBBP7	47,8	5,05	0,60
108	Q6YN16	Hydroxysteroid dehydrogenase-like protein 2	HSDL2	45,4	7,99	0,64
109	O00629	Importin subunit alpha-3	KPNA4	57,9	4,96	0,66
110	O60684	Importin subunit alpha-7	KPNA6	60,0	4,98	2,02
111	Q8TEX9	Importin-4	IPO4	118,6	4,96	1,98
112	Q96P70	Importin-9	IPO9	115,9	4,81	1,56
113	P05556	Integrin beta-1	ITGB1	88,4	5,39	0,65
114	Q13418	Integrin-linked protein kinase	ILK	51,4	8,07	0,57
115	O94819	Kelch repeat and BTB domain-containing protein 11	KBTBD11	65,7	6,07	1,52
116	Q96EK5	KIF1-binding protein	KIF1BP	71,8	5,49	runter
117	O60488	Long-chain-fatty-acid--CoA ligase 4	ACSL4	79,1	8,38	0,57
118	Q9Y4K0	Lysyl oxidase homolog 2	LOXL2	86,7	6,38	hoch
119	Q9ULC4	Malignant T-cell-amplified sequence 1	MCTS1	20,5	8,82	2,23
120	Q3KQU3	MAP7 domain-containing protein 1	MAP7D1	92,8	10,11	2,01
121	Q9UNF1	Melanoma-associated antigen D2	MAGED2	64,9	9,32	1,53

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
122	O00264	Membrane-associated progesterone receptor component 1	PGRMC1	21,7	4,70	1,58
123	O94776	Metastasis-associated protein MTA2	MTA2	75,0	9,66	2,65
124	Q7L0Y3	Mitochondrial ribonuclease P protein 1	TRMT10C	47,3	9,36	hoch
125	Q10713	Mitochondrial-processing peptidase subunit alpha	PMPCA	58,2	6,92	1,54
126	P27361	Mitogen-activated protein kinase 3	MAPK3	43,1	6,74	0,57
127	Q9Y6D9	Mitotic spindle assembly checkpoint protein MAD1	MAD1L1	83,0	5,92	runter
128	P84022	Mothers against decapentaplegic homolog 3	SMAD3	48,1	7,15	hoch
129	O43148	mRNA cap guanine-N7 methyltransferase	RNMT	54,8	6,61	0,59
130	O15439	Multidrug resistance-associated protein 4	ABCC4	149,4	8,19	1,50
131	Q9BQG0	Myb-binding protein 1A	MYBBP1A	148,8	9,28	2,00
132	Q9UJ70	N-acetyl-D-glucosamine kinase	NAGK	37,4	6,24	hoch
133	O75251	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	23,5	9,99	0,62
134	Q9GZZ1	N-alpha-acetyltransferase 50	NAA50	19,4	8,81	0,64
135	Q8TBC4	NEDD8-activating enzyme E1 catalytic subunit	UBA3	51,8	5,45	3,16
136	Q9BYT8	Neurolysin, mitochondrial	NLN	80,6	6,64	0,61
137	Q969V3	Nicalin	NCLN	62,9	6,89	0,66
138	**P40261**	**Nicotinamide N-methyltransferase**	**NNMT**	**29,6**	**5,74**	**5,43**
139	P43490	Nicotinamide phosphoribosyltransferase	NAMPT	55,5	7,15	2,10
140	P22307	Non-specific lipid-transfer protein	SCP2	59,0	6,89	0,56
141	P57740	Nuclear pore complex protein Nup107	NUP107	106,3	5,43	0,54
142	P37198	Nuclear pore glycoprotein p62	NUP62	53,2	5,31	0,57
143	Q02818	Nucleobindin-1	NUCB1	53,8	5,25	1,56
144	Q14978	Nucleolar and coiled-body phosphoprotein 1	NOLC1	73,6	9,47	1,87
145	P15531	Nucleoside diphosphate kinase A	NME1	17,1	6,19	0,56
146	Q9NQR4	Omega-amidase NIT2	NIT2	30,6	7,21	0,60
147	P04181	Ornithine aminotransferase, mitochondrial	OAT	48,5	7,03	0,60
148	O75475	PC4 and SFRS1-interacting protein	PSIP1	60,1	9,13	hoch
149	Q08752	Peptidyl-prolyl cis-trans isomerase D	PPID	40,7	7,21	runter
150	P62942	Peptidyl-prolyl cis-trans isomerase FKBP1A	FKBP1A	11,9	8,16	0,54
151	O95302	Peptidyl-prolyl cis-trans isomerase FKBP9	FKBP9	63,0	5,08	2,26
152	Q8IWS0	PHD finger protein 6	PHF6	41,3	8,68	2,43
153	P48651	Phosphatidylserine synthase 1	PTDSS1	55,5	8,43	1,50
154	Q96G03	Phosphoglucomutase-2	PGM2	68,2	6,73	0,52
155	Q96BW5	Phosphotriesterase-related protein	PTER	39,0	6,52	0,47
156	Q9UKK3	Poly [ADP-ribose] polymerase 4	PARP4	192,5	5,66	4,57
157	Q86U42	Polyadenylate-binding protein 2	PABPN1	32,7	5,06	0,63
158	P61758	Prefoldin subunit 3	VBP1	22,6	7,11	1,74

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
159	Q6P2Q9	Pre-mRNA-processing-splicing factor 8	PRPF8	273,4	8,84	0,59
160	Q8IY21	Probable ATP-dependent RNA helicase DDX60	DDX60	197,7	7,59	2,29
161	P49590	Probable histidine--tRNA ligase, mitochondrial	HARS2	56,9	8,24	1,60
162	P35232	Prohibitin	PHB	29,8	5,76	4,52
163	O15460	Prolyl 4-hydroxylase subunit alpha-2	P4HA2	60,9	5,71	0,46
164	Q9H7Z7	Prostaglandin E synthase 2	PTGES2	41,9	9,16	hoch
165	P28070	Proteasome subunit beta type-4	PSMB4	29,2	5,97	0,56
166	Q8NCA5	Protein FAM98A	FAM98A	55,4	9,03	hoch
167	Q9UNF0	Protein kinase C and casein kinase substrate in neurons protein 2	PACSIN2	55,7	5,20	0,55
168	Q9BZQ8	Protein Niban	FAM129A	103,1	4,78	7,58
169	O75323	Protein NipSnap homolog 2	GBAS	33,7	9,36	hoch
170	O14974	Protein phosphatase 1 regulatory subunit 12A	PPP1R12A	115,2	5,40	1,65
171	P41236	Protein phosphatase inhibitor 2	PPP1R2	23,0	4,74	0,48
172	Q6NXS1	Protein phosphatase inhibitor 2-like protein 3	PPP1R2P3	23,0	4,92	0,48
173	Q9H3U1	Protein unc-45 homolog A	UNC45A	103,0	6,07	0,53
174	P12931	Proto-oncogene tyrosine-protein kinase Src	SRC	59,8	7,42	0,64
175	P61457	Pterin-4-alpha-carbinolamine dehydratase	PCBD1	12,0	6,80	1,89
176	Q58FG0	Putative heat shock protein HSP 90-alpha A5	HSP90AA5P	38,7	6,57	2,79
177	Q6P996	Pyridoxal-dependent decarboxylase domain-containing protein 1	PDXDC1	86,7	5,38	1,57
178	O00330	Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	54,1	8,66	hoch
179	Q9H6Z4	Ran-binding protein 3	RANBP3	60,2	4,78	0,51
180	P61106	Ras-related protein Rab-14	RAB14	23,9	6,21	1,66
181	Q9NQG5	Regulation of nuclear pre-mRNA domain-containing protein 1B	RPRD1B	36,9	5,97	0,17
182	P27694	Replication protein A 70 kDa DNA-binding subunit	RPA1	68,1	7,21	runter
183	P00352	Retinal dehydrogenase 1	ALDH1A1	54,8	6,73	0,59
184	Q99575	Ribonucleases P/MRP protein subunit POP1	POP1	114,6	9,22	1,69
185	Q08AF3	Schlafen family member 5	SLFN5	101,0	8,22	1,65
186	Q16629	Serine/arginine-rich splicing factor 7	SRSF7	27,4	11,82	1,56
187	Q9P289	Serine/threonine-protein kinase 26	STK26	46,5	5,29	0,65
188	Q08209	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	PPP3CA	58,7	5,86	2,90
189	P16298	Serine/threonine-protein phosphatase 2B catalytic subunit beta isoform	PPP3CB	59,0	5,91	2,90
190	Q9BRF8	Serine/threonine-protein phosphatase CPPED1	CPD1	35,5	6,20	0,43
191	P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	PPP1CB	37,2	6,19	runter
192	Q9BXP5	Serrate RNA effector molecule homolog	SRRT	100,6	5,96	1,88

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
193	Q9NR45	Sialic acid synthase	NANS	40,3	6,74	1,56
194	Q15005	Signal peptidase complex subunit 2	SPCS2	25,0	8,47	runter
195	P08240	Signal recognition particle receptor subunit alpha	SRPRA	69,8	8,95	0,19
196	O76094	Signal recognition particle subunit SRP72	SRP72	74,6	9,26	4,30
197	P63162	Small nuclear ribonucleoprotein-associated protein N	SNRPN	24,6	11,19	3,16
198	P14678	Small nuclear ribonucleoprotein-associated proteins B and B'	SNRPB	24,6	11,19	3,16
199	P05026	Sodium/potassium-transporting ATPase subunit beta-1	ATP1B1	35,0	8,53	4,53
200	P11166	Solute carrier family 2, facilitated glucose transporter member 1	SLC2A1	54,0	8,72	0,44
201	P52788	Spermine synthase	SMS	41,2	5,02	2,06
202	Q96I25	Splicing factor 45	RBM17	44,9	5,97	2,02
203	P23246	Splicing factor, proline- and glutamine-rich	SFPQ	76,1	9,44	1,54
204	Q9H2G2	STE20-like serine/threonine-protein kinase	SLK	142,6	5,15	0,61
205	O95347	Structural maintenance of chromosomes protein 2	SMC2	135,6	8,43	0,51
206	Q9NTJ3	Structural maintenance of chromosomes protein 4	SMC4	147,1	6,79	1,81
207	P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB	31,6	8,76	1,58
208	P42285	Superkiller viralicidic activity 2-like 2	SKIV2L2	117,7	6,52	4,25
209	Q969G3	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	SMARCE1	46,6	4,88	7,45
210	O95881	Thioredoxin domain-containing protein 12	TXNDC12	19,2	5,40	0,65
211	P19971	Thymidine phosphorylase	TYMP	49,9	5,53	1,96
212	P20290	Transcription factor BTF3	BTF3	22,2	9,38	0,64
213	Q96K17	Transcription factor BTF3 homolog 4	BTF3L4	17,3	6,35	runter
214	Q04206	Transcription factor p65	RELA	60,2	5,68	runter
215	P46937	Transcriptional coactivator YAP1	YAP1	54,4	5,17	runter
216	Q99598	Translin-associated protein X	TSNAX	33,1	6,55	1,55
217	P49755	Transmembrane emp24 domain-containing protein 10	TMED10	25,0	7,44	2,44
218	Q9BVK6	Transmembrane emp24 domain-containing protein 9	TMED9	27,3	8,02	2,59
219	Q9BTV4	Transmembrane protein 43	TMEM43	44,8	8,13	0,33
220	Q13428	Treacle protein	TCOF1	152,0	9,04	2,29
221	P53007	Tricarboxylate transport protein, mitochondrial	SLC25A1	34,0	9,89	hoch
222	Q15813	Tubulin-specific chaperone E	TBCE	59,3	6,76	hoch
223	P25445	Tumor necrosis factor receptor superfamily member 6	FAS	37,7	7,94	2,34
224	P07947	Tyrosine-protein kinase Yes	YES1	60,8	6,74	1,92
225	P08621	U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70	51,5	9,94	0,56
226	O43172	U4/U6 small nuclear ribonucleoprotein Prp4	PRPF4	58,4	7,42	0,53
227	Q9Y4E8	Ubiquitin carboxyl-terminal hydrolase 15	USP15	112,3	5,22	1,54

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
228	Q93009	Ubiquitin carboxyl-terminal hydrolase 7	USP7	128,2	5,55	2,09
229	P09936	Ubiquitin carboxyl-terminal hydrolase isozyme L1	UCHL1	24,8	5,48	0,64
230	Q13404	Ubiquitin-conjugating enzyme E2 variant 1	UBE2V1	16,5	7,93	0,66
231	Q9HAW9	UDP-glucuronosyltransferase 1-8	UGT1A8	59,7	7,68	runter
232	Q16222	UDP-N-acetylhexosamine pyrophosphorylase	UAP1	58,7	6,33	hoch
233	Q9UM54	Unconventional myosin-VI	MYO6	149,6	8,53	1,88
234	Q96QK1	Vacuolar protein sorting-associated protein 35	VPS35	91,6	5,49	1,57
235	Q53GQ0	Very-long-chain 3-oxoacyl-CoA reductase	HSD17B12	34,3	9,32	hoch
236	P61964	WD repeat-containing protein 5	WDR5	36,6	8,27	1,90

Tabelle S10: Differenziell exprimierte Proteine von transient transfizierten 769-P Zellen bei 20 µM Methionin (mock *vs*. NNMT)

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
1	P43686	26S protease regulatory subunit 6B	PSMC4	47,3	5,21	runter
2	P51665	26S proteasome non-ATPase regulatory subunit 7	PSMD7	37,0	6,77	10,33
3	P51398	28S ribosomal protein S29, mitochondrial	DAP3	45,5	8,88	0,56
4	Q9Y2R9	28S ribosomal protein S7, mitochondrial	MRPS7	28,1	9,99	0,30
5	Q96A35	39S ribosomal protein L24, mitochondrial	MRPL24	24,9	9,29	runter
6	Q9BRK5	45 kDa calcium-binding protein	SDF4	41,8	4,86	hoch
7	P46779	60S ribosomal protein L28	RPL28	15,7	12,02	1,56
8	P68032	Actin, alpha cardiac muscle 1	ACTC1	42,0	5,39	1,94
9	P68133	Actin, alpha skeletal muscle	ACTA1	42,0	5,39	1,94
10	P62736	Actin, aortic smooth muscle	ACTA2	42,0	5,39	1,94
11	P54819	Adenylate kinase 2, mitochondrial	AK2	26,5	7,81	0,37
12	P40123	Adenylyl cyclase-associated protein 2	CAP2	52,8	6,37	hoch
13	Q9BW91	ADP-ribose pyrophosphatase, mitochondrial	NUDT9	39,1	8,22	1,64
14	P30837	Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	57,2	6,80	0,59
15	P02511	Alpha-crystallin B chain	CRYAB	20,1	7,33	0,56
16	P15144	Aminopeptidase N	ANP	109,5	5,48	0,53
17	P08133	Annexin A6	ANXA6	75,8	5,60	9,23
18	Q03518	Antigen peptide transporter 1	TAP1	87,2	8,02	1,65
19	O95782	AP-2 complex subunit alpha-1	AP2A1	107,5	7,03	1,74
20	Q9ULA0	Aspartyl aminopeptidase	DNP	52,4	7,42	0,63
21	Q15121	Astrocytic phosphoprotein PEA-15	A15	15,0	5,02	1,69
22	Q5T2N8	ATPase family AAA domain-containing protein 3C	ATAD3C	46,4	9,31	0,46
23	Q8NE71	ATP-binding cassette sub-family F member 1	ABCF1	95,9	6,80	3,90

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
24	P08237	ATP-dependent 6-phosphofructokinase, muscle type	PFKM	85,1	7,99	1,81
25	Q9NVP1	ATP-dependent RNA helicase DDX18	DDX18	75,4	9,50	0,59
26	Q7L1Q6	Basic leucine zipper and W2 domain-containing protein 1	BZW1	48,0	5,92	8,77
27	Q9NYF8	Bcl-2-associated transcription factor 1	BCLAF1	106,1	9,98	0,45
28	Q562R1	Beta-actin-like protein 2	ACTBL2	42,0	5,59	0,07
29	P53004	Biliverdin reductase A	BLVRA	33,4	6,44	0,63
30	Q13867	Bleomycin hydrolase	BLMH	52,5	6,27	hoch
31	Q9Y6D6	Brefeldin A-inhibited guanine nucleotide-exchange protein 1	ARFGEF1	208,6	5,85	0,39
32	O75844	CAAX prenyl protease 1 homolog	ZMPSTE24	54,8	7,49	1,53
33	O43852	Calumenin	CALU	37,1	4,64	0,63
34	P13861	cAMP-dependent protein kinase type II-alpha regulatory subunit	PRKAR2A	45,5	5,07	runter
35	O60716	Catenin delta-1	CTNND1	108,1	6,23	1,50
36	P20645	Cation-dependent mannose-6-phosphate receptor	M6PR	31,0	5,83	0,64
37	P32970	CD70 antigen	CD70	21,1	8,53	2,03
38	Q15642	Cdc42-interacting protein 4	TRIP10	68,3	5,73	1,79
39	O43809	Cleavage and polyadenylation specificity factor subunit 5	NUDT21	26,2	8,82	hoch
40	Q12996	Cleavage stimulation factor subunit 3	CSTF3	82,9	8,12	1,71
41	Q14019	Coactosin-like protein	COTL1	15,9	5,67	0,47
42	Q96A33	Coiled-coil domain-containing protein 47	CCDC47	55,8	4,87	2,80
43	Q13618	Cullin-3	CUL3	88,9	8,48	0,55
44	Q00534	Cyclin-dependent kinase 6	CDK6	36,9	6,46	0,64
45	Q16527	Cysteine and glycine-rich protein 2	CSRP2	20,9	8,62	runter
46	Q9UHD1	Cysteine and histidine-rich domain-containing protein 1	CHORDC1	37,5	7,87	runter
47	Q14008	Cytoskeleton-associated protein 5	CKAP5	225,4	7,80	0,60
48	Q96GG9	DCN1-like protein 1	DCUN1D1	30,1	5,34	hoch
49	Q9H773	dCTP pyrophosphatase 1	DCTPP1	18,7	5,03	0,52
50	P33316	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial	DUT	26,5	9,36	1,65
51	Q99543	DnaJ homolog subfamily C member 2	DNAJC2	72,0	8,70	0,61
52	Q9UHG0	Doublecortin domain-containing protein 2	DCDC2	52,8	6,13	0,56
53	O95793	Double-stranded RNA-binding protein Staufen homolog 1	STAU1	63,1	9,44	2,30
54	Q9UII4	E3 ISG15--protein ligase HERC5	HERC5	116,8	7,65	2,31
55	Q9P0J7	E3 ubiquitin-protein ligase KCMF1	KCMF1	41,9	5,66	2,10
56	Q8IUD2	ELKS/Rab6-interacting/CAST family member 1	ERC1	128,0	5,97	runter
57	Q6P179	Endoplasmic reticulum aminopeptidase 2	ERAP2	110,4	6,71	1,68
58	O75477	Erlin-1	ERLIN1	38,9	7,87	0,27
59	Q9UBQ5	Eukaryotic translation initiation factor 3 subunit K	EIF3K	25,0	4,93	1,83

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
60	P23588	Eukaryotic translation initiation factor 4B	EIF4B	69,1	5,73	1,56
61	Q96I24	Far upstream element-binding protein 3	FUBP3	61,6	8,38	0,62
62	P14324	Farnesyl pyrophosphate synthase	FDPS	48,2	6,15	runter
63	P02792	Ferritin light chain	FTL	20,0	5,78	runter
64	Q14254	Flotillin-2	FLOT2	47,0	5,25	1,62
65	P16930	Fumarylacetoacetase	FAH	46,3	6,95	0,63
66	O75223	Gamma-glutamylcyclotransferase	GGCT	21,0	5,14	runter
67	P57764	Gasdermin-D	GSDMD	52,8	5,08	1,60
68	P14314	Glucosidase 2 subunit beta	PRKCSH	59,4	4,41	2,01
69	P23378	Glycine dehydrogenase (decarboxylating), mitochondrial	GLDC	112,7	7,11	8,73
70	Q9BVP2	Guanine nucleotide-binding protein-like 3	GNL3	62,0	9,16	0,56
71	P17096	High mobility group protein HMG-I/HMG-Y	HMGA1	11,7	10,32	1,84
72	P52926	High mobility group protein HMGI-C	HMGA2	11,8	10,62	1,70
73	O00629	Importin subunit alpha-3	KPNA4	57,9	4,96	2,51
74	O60684	Importin subunit alpha-7	KPNA6	60,0	4,98	0,62
75	P07942	Laminin subunit beta-1	LAMB1	197,9	4,94	0,65
76	O95202	LETM1 and EF-hand domain-containing protein 1, mitochondrial	LETM1	83,3	6,70	0,54
77	Q9BTE3	Mini-chromosome maintenance complex-binding protein	MCMBP	72,9	5,87	runter
78	O60220	Mitochondrial import inner membrane translocase subunit Tim8 A	TIMM8A	11,0	5,16	runter
79	O75439	Mitochondrial-processing peptidase subunit beta	PMPCB	54,3	6,83	1,56
80	P28482	Mitogen-activated protein kinase 1	MAPK1	41,4	6,98	1,77
81	Q16539	Mitogen-activated protein kinase 14	MAPK14	41,3	5,78	0,60
82	P27361	Mitogen-activated protein kinase 3	MAPK3	43,1	6,74	1,59
83	Q9NUJ1	Mycophenolic acid acyl-glucuronide esterase, mitochondrial	ABHD10	33,9	8,57	runter
84	O95299	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	40,7	8,48	2,11
85	P48163	NADP-dependent malic enzyme	ME1	64,1	6,13	0,60
86	Q13564	NEDD8-activating enzyme E1 regulatory subunit	NAE1	60,2	5,40	0,49
87	**P40261**	**Nicotinamide N-methyltransferase**	**NNMT**	**29,6**	**5,74**	**13,65**
88	Q15155	Nodal modulator 1	NOMO1	134,2	5,81	0,66
89	Q5JPE7	Nodal modulator 2	NOMO2	139,4	5,76	0,66
90	P69849	Nodal modulator 3	NOMO3	134,0	5,67	0,66
91	P57740	Nuclear pore complex protein Nup107	NUP107	106,3	5,43	0,66
92	P52948	Nuclear pore complex protein Nup98-Nup96	NUP98	197,5	6,40	2,03
93	Q8TEM1	Nuclear pore membrane glycoprotein 210	NUP210	205,0	6,81	0,66
94	Q14978	Nucleolar and coiled-body phosphoprotein 1	NOLC1	73,6	9,47	1,57

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
95	Q01085	Nucleolysin TIAR	TIAL1	41,6	7,74	hoch
96	Q8NFH5	Nucleoporin NUP53	NUP35	34,8	9,09	0,59
97	Q9BQ69	O-acetyl-ADP-ribose deacetylase MACROD1	MACROD1	35,5	9,51	1,52
98	Q15645	Pachytene checkpoint protein 2 homolog	TRIP13	48,5	6,09	hoch
99	Q06710	Paired box protein Pax-8	PAX8	48,2	7,84	0,65
100	O75475	PC4 and SFRS1-interacting protein	PSIP1	60,1	9,13	1,53
101	O00151	PDZ and LIM domain protein 1	PDLIM1	36,0	7,02	0,64
102	Q96EY7	Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	78,5	6,42	0,41
103	P62942	Peptidyl-prolyl cis-trans isomerase FKBP1A	FKBP1A	11,9	8,16	0,53
104	Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3	FKBP3	25,2	9,28	2,01
105	Q8IWS0	PHD finger protein 6	PHF6	41,3	8,68	1,50
106	Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	70,7	7,62	0,64
107	O95758	Polypyrimidine tract-binding protein 3	PTBP3	59,7	9,04	runter
108	Q96AQ6	Pre-B-cell leukemia transcription factor-interacting protein 1	PBXIP1	80,6	5,33	hoch
109	O94903	Proline synthase co-transcribed bacterial homolog protein	PROSC	30,3	7,50	hoch
110	P28070	Proteasome subunit beta type-4	PSMB4	29,2	5,97	0,34
111	Q8NCA5	Protein FAM98A	FAM98A	55,4	9,03	1,76
112	Q9UFN0	Protein NipSnap homolog 3A	NIPSNAP3A	28,4	9,16	2,05
113	Q9P258	Protein RCC2	RCC2	56,0	8,78	0,59
114	Q58FG0	Putative heat shock protein HSP 90-alpha A5	HSP90AA5P	38,7	6,57	0,52
115	B2RPK0	Putative high mobility group protein B1-like 1	HMGB1P1	24,2	6,21	1,76
116	Q6P996	Pyridoxal-dependent decarboxylase domain-containing protein 1	PDXDC1	86,7	5,38	4,24
117	P08559	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	43,3	8,06	runter
118	P35241	Radixin	RDX	68,5	6,37	2,09
119	P52306	Rap1 GTPase-GDP dissociation stimulator 1	RAP1GDS1	66,3	5,31	1,72
120	Q15286	Ras-related protein Rab-35	RAB35	23,0	8,29	0,62
121	P61006	Ras-related protein Rab-8A	RAB8A	23,7	9,07	4,18
122	P11234	Ras-related protein Ral-B	RALB	23,4	6,62	1,51
123	Q9NQG5	Regulation of nuclear pre-mRNA domain-containing protein 1B	RPRD1B	36,9	5,97	runter
124	P35250	Replication factor C subunit 2	RFC2	39,1	6,44	runter
125	Q9NQC3	Reticulon-4	RTN4	129,9	4,50	0,57
126	Q7LG56	Ribonucleoside-diphosphate reductase subunit M2 B	RRM2B	40,7	4,97	3,41
127	P51812	Ribosomal protein S6 kinase alpha-3	RPS6KA3	83,7	6,89	runter
128	Q96E11	Ribosome-recycling factor, mitochondrial	MRRF	29,3	9,79	1,62
129	Q15424	Scaffold attachment factor B1	SAFB	102,6	5,47	0,64

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	Faktor mock *vs*. NNMT
130	Q9BRF8	Serine/threonine-protein phosphatase CPPED1	CPD1	35,5	6,20	1,57
131	P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	PPP1CB	37,2	6,19	7,87
132	Q15005	Signal peptidase complex subunit 2	SPCS2	25,0	8,47	0,59
133	P08240	Signal recognition particle receptor subunit alpha	SRPRA	69,8	8,95	runter
134	P05026	Sodium/potassium-transporting ATPase subunit beta-1	ATP1B1	35,0	8,53	0,36
135	O60493	Sorting nexin-3	SNX3	18,8	8,66	0,53
136	Q9H2G2	STE20-like serine/threonine-protein kinase	SLK	142,6	5,15	1,51
137	Q9UBE0	SUMO-activating enzyme subunit 1	SAE1	38,4	5,30	2,23
138	P63279	SUMO-conjugating enzyme UBC9	UBE2I	18,0	8,66	1,88
139	P42285	Superkiller viralicidic activity 2-like 2	SKIV2L2	117,7	6,52	hoch
140	Q12846	Syntaxin-4	STX4	34,2	6,28	hoch
141	O43493	Trans-Golgi network integral membrane protein 2	TGOLN2	51,1	5,73	0,56
142	Q13509	Tubulin beta-3 chain	TUBB3	50,4	4,93	1,50
143	P04350	Tubulin beta-4A chain	TUBB4A	49,6	4,88	2,22
144	O43172	U4/U6 small nuclear ribonucleoprotein Prp4	PRPF4	58,4	7,42	2,08
145	Q93009	Ubiquitin carboxyl-terminal hydrolase 7	USP7	128,2	5,55	2,54
146	P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3	UCHL3	26,2	4,92	1,51
147	Q9HAW9	UDP-glucuronosyltransferase 1-8	UGT1A8	59,7	7,68	runter
148	P46939	Utrophin	UTRN	394,2	5,33	0,37
149	O75436	Vacuolar protein sorting-associated protein 26A	VPS26A	38,1	6,57	1,59
150	Q9NP79	Vacuolar protein sorting-associated protein VTA1 homolog	VTA1	33,9	6,29	3,99
151	P21283	V-type proton ATPase subunit C 1	ATP6V1C1	43,9	7,46	runter
152	Q9UNX4	WD repeat-containing protein 3	WDR3	106,0	6,64	hoch
153	Q9GZS3	WD repeat-containing protein 61	WDR61	33,6	5,47	1,76
154	Q9Y6W5	Wiskott-Aldrich syndrome protein family member 2	WASF2	54,3	5,53	0,44

Tabelle S11: Gemeinsame differenziell exprimierte Proteine von transient transfizierten HEK-293 Zellen bei 100 µM und 20 µM Methionin (mock *vs*. NNMT)

						Faktor mock *vs.* NNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**HEK-293 100 µM**	**HEK-293 20 µM**
1	P12694	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	BCKDHA	50,4	8,27	0,65	runter
2	P62841	40S ribosomal protein S15	RPS15	17,0	10,39	1,51	0,54
3	P62249	40S ribosomal protein S16	RPS16	16,4	10,21	1,80	0,64
4	P23396	40S ribosomal protein S3	RPS3	26,7	9,66	1,77	0,62
5	P07108	Acyl-CoA-binding protein	DBI	10,0	6,57	0,32	0,52
6	P55263	Adenosine kinase	ADK	40,5	6,70	runter	1,70
7	P84077	ADP-ribosylation factor 1	ARF1	20,7	6,80	1,70	0,52
8	P61204	ADP-ribosylation factor 3	ARF3	20,6	7,43	1,70	0,52
9	Q9UBB4	Ataxin-10	ATXN10	53,5	5,25	0,64	0,61
10	P28288	ATP-binding cassette sub-family D member 3	ABCD3	75,4	9,36	0,55	1,93
11	Q9UMR2	ATP-dependent RNA helicase DDX19B	DDX19B	53,9	6,30	0,66	0,58
12	Q9Y6E2	Basic leucine zipper and W2 domain-containing protein 2	BZW2	48,1	6,68	3,46	runter
13	P55957	BH3-interacting domain death agonist	BID	22,0	5,44	1,72	0,65
14	P42574	Caspase-3	CASP3	31,6	6,54	0,54	0,38
15	O43809	Cleavage and polyadenylation specificity factor subunit 5	NUDT21	26,2	8,82	1,61	0,27
16	P35606	Coatomer subunit beta'	COPB2	102,4	5,27	0,58	1,56
17	Q13363	C-terminal-binding protein 1	CTBP1	47,5	6,77	1,50	1,91
18	O43175	D-3-phosphoglycerate dehydrogenase	PHGDH	56,6	6,71	1,59	0,63
19	Q14203	Dynactin subunit 1	DCTN1	141,6	5,81	0,64	2,11
20	O60313	Dynamin-like 120 kDa protein, mitochondrial	OPA1	111,6	7,87	1,52	runter
21	P63167	Dynein light chain 1, cytoplasmic	DYNLL1	10,4	7,40	0,29	0,50
22	Q99496	E3 ubiquitin-protein ligase RING2	RNF2	37,6	6,84	1,70	runter
23	Q96C19	EF-hand domain-containing protein D2	EFHD2	26,7	5,20	0,40	21,40
24	P55884	Eukaryotic translation initiation factor 3 subunit B	EIF3B	92,4	5,00	1,67	1,56
25	P23588	Eukaryotic translation initiation factor 4B	EIF4B	69,1	5,73	0,45	0,64
26	P28161	Glutathione S-transferase Mu 2	GSTM2	25,7	6,37	1,66	runter
27	Q9H4A6	Golgi phosphoprotein 3	GOLPH3	33,8	6,44	0,61	2,91
28	Q12849	G-rich sequence factor 1	GRSF1	53,1	6,19	runter	0,45
29	P51858	Hepatoma-derived growth factor	HDGF	26,8	4,73	0,63	0,56
30	Q7Z4V5	Hepatoma-derived growth factor-related protein 2	HDGFRP2	74,3	7,49	2,30	0,55
31	Q9NSK0	Kinesin light chain 4	KLC4	68,6	6,18	runter	0,65
32	P55081	Microfibrillar-associated protein 1	MFAP1	51,9	4,98	1,57	0,59

						Faktor mock vs. NNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**HEK-293 100 µM**	**HEK-293 20 µM**
33	Q9Y3A3	MOB-like protein phocein	MOB4	26,0	5,78	4,28	hoch
34	P48163	NADP-dependent malic enzyme	ME1	64,1	6,13	1,74	hoch
35	Q8WX92	Negative elongation factor B	NELFB	65,7	6,13	hoch	hoch
36	Q96TA1	Niban-like protein 1	FAM129B	84,1	6,19	runter	2,53
37	**P40261**	**Nicotinamide N-methyltransferase**	**NNMT**	**29,6**	**5,74**	**hoch**	**hoch**
38	Q15155	Nodal modulator 1	NOMO1	134,2	5,81	0,45	1,70
39	Q5JPE7	Nodal modulator 2	NOMO2	139,4	5,76	0,45	1,70
40	P69849	Nodal modulator 3	NOMO3	134,0	5,67	0,45	1,70
41	P57740	Nuclear pore complex protein Nup107	NUP107	106,3	5,43	0,39	0,51
42	Q9UKX7	Nuclear pore complex protein Nup50	NUP50	50,1	7,06	1,67	0,54
43	Q14978	Nucleolar and coiled-body phosphoprotein 1	NOLC1	73,6	9,47	2,80	0,63
44	O75475	PC4 and SFRS1-interacting protein	PSIP1	60,1	9,13	1,63	0,50
45	P26885	Peptidyl-prolyl cis-trans isomerase FKBP2	FKBP2	15,6	9,13	2,07	0,66
46	Q9UHG3	Prenylcysteine oxidase 1	PCYOX1	56,6	6,18	0,48	2,15
47	Q14914	Prostaglandin reductase 1	PTGR1	35,8	8,29	1,72	0,50
48	P49721	Proteasome subunit beta type-2	PSMB2	22,8	7,02	2,07	runter
49	Q99873	Protein arginine N-methyltransferase 1	PRMT1	41,5	5,43	1,54	1,76
50	Q15435	Protein phosphatase 1 regulatory subunit 7	PPP1R7	41,5	4,91	1,90	0,63
51	P31949	Protein S100-A11	S100A11	11,7	7,12	0,35	runter
52	Q14671	Pumilio homolog 1	PUM1	126,4	6,84	0,60	runter
53	B2RPK0	Putative high mobility group protein B1-like 1	HMGB1P1	24,2	6,21	1,74	0,52
54	P51149	Ras-related protein Rab-7a	RAB7A	23,5	6,70	1,71	0,65
55	P61006	Ras-related protein Rab-8A	RAB8A	23,7	9,07	1,57	0,34
56	P98179	RNA-binding protein 3	RBM3	17,2	8,91	0,55	0,47
57	Q15424	Scaffold attachment factor B1	SAFB	102,6	5,47	0,64	0,59
58	Q16629	Serine/arginine-rich splicing factor 7	SRSF7	27,4	11,82	0,56	4,09
59	Q9Y5M8	Signal recognition particle receptor subunit beta	SRPRB	29,7	9,04	hoch	0,57
60	Q13573	SNW domain-containing protein 1	SNW1	61,5	9,52	1,72	runter
61	O60493	Sorting nexin-3	SNX3	18,8	8,66	runter	0,38
62	Q8N0X7	Spartin	SPG20	72,8	5,91	2,00	0,61
63	P35610	Sterol O-acyltransferase 1	SOAT1	64,7	8,94	1,94	1,61
64	Q9UJZ1	Stomatin-like protein 2, mitochondrial	STOML2	38,5	7,39	1,56	0,53
65	O95347	Structural maintenance of chromosomes protein 2	SMC2	135,6	8,43	2,03	0,43
66	P63279	SUMO-conjugating enzyme UBC9	UBE2I	18,0	8,66	1,69	0,46
67	Q969G3	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	SMARCE1	46,6	4,88	5,16	8,26
68	O00161	Synaptosomal-associated protein 23	SNAP23	23,3	5,01	runter	0,55

						Faktor mock vs. NNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**HEK-293 100 µM**	**HEK-293 20 µM**
69	Q86YP4	Transcriptional repressor p66-alpha	GATAD2A	68,0	9,94	runter	runter
70	P02786	Transferrin receptor protein 1	TFRC	84,8	6,61	0,58	1,55
71	Q9BTV4	Transmembrane protein 43	TMEM43	44,8	8,13	0,52	runter
72	Q7Z2T5	TRMT1-like protein	TRMT1L	81,7	7,88	1,69	2,95
73	P04350	Tubulin beta-4A chain	TUBB4A	49,6	4,88	5,10	2,33
74	Q9UMX0	Ubiquilin-1	UBQLN1	62,5	5,11	0,64	0,63
75	Q93009	Ubiquitin carboxyl-terminal hydrolase 7	USP7	128,2	5,55	0,25	1,56
76	O75396	Vesicle-trafficking protein SEC22b	SEC22B	24,6	6,92	1,52	2,21
77	P12955	Xaa-Pro dipeptidase	PD	54,5	6,00	0,61	1,72

Tabelle S12: Gemeinsame differenziell exprimierte Proteine von transient transfizierten Caki-2 Zellen bei 100 µM und 20 µM Methionin (mock vs. NNMT)

						Faktor mock *vs.* NNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**Caki-2 100 µM**	**Caki-2 20 µM**
1	P51665	26S proteasome non-ATPase regulatory subunit 7	PSMD7	37,0	6,77	2,88	runter
2	Q9BRJ2	39S ribosomal protein L45, mitochondrial	MRPL45	35,3	9,03	1,68	hoch
3	P25325	3-mercaptopyruvate sulfurtransferase	MPST	33,2	6,60	1,52	hoch
4	P08708	40S ribosomal protein S17	RPS17	15,5	9,85	0,60	1,71
5	P62750	60S ribosomal protein L23a	RPL23A	17,7	10,45	0,62	0,54
6	P61254	60S ribosomal protein L26	RPL26	17,2	10,55	1,55	1,54
7	P54819	Adenylate kinase 2, mitochondrial	AK2	26,5	7,81	1,63	0,34
8	P84077	ADP-ribosylation factor 1	ARF1	20,7	6,80	0,64	0,50
9	P61204	ADP-ribosylation factor 3	ARF3	20,6	7,43	0,64	0,50
10	P52895	Aldo-keto reductase family 1 member C2	AKR1C2	36,7	7,49	0,53	0,59
11	Q15121	Astrocytic phosphoprotein PEA-15	A15	15,0	5,02	0,57	0,64
12	Q9NVI7	ATPase family AAA domain-containing protein 3A	ATAD3A	71,3	8,98	2,55	0,58
13	Q5T2N8	ATPase family AAA domain-containing protein 3C	ATAD3C	46,4	9,31	1,61	0,33
14	O75531	Barrier-to-autointegration factor	BANF1	10,1	6,09	0,58	2,30
15	Q9Y6E2	Basic leucine zipper and W2 domain-containing protein 2	BZW2	48,1	6,68	0,58	runter
16	P42025	Beta-centractin	ACTR1B	42,3	6,40	runter	0,55
17	Q6NUK1	Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	53,3	6,33	2,61	1,80
18	Q05682	Caldesmon	CALD1	93,2	5,66	0,47	runter
19	O75828	Carbonyl reductase [NADPH] 3	CBR3	30,8	6,18	0,49	1,98

						Faktor mock vs. NNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**Caki-2 100 µM**	**Caki-2 20 µM**
20	P04040	Catalase	CAT	59,7	7,39	0,52	2,00
21	Q96CT7	Coiled-coil domain-containing protein 124	CCDC124	25,8	9,54	runter	1,55
22	Q9UBG0	C-type mannose receptor 2	MRC2	166,6	5,83	0,53	runter
23	Q7L576	Cytoplasmic FMR1-interacting protein 1	CYFIP1	145,1	6,90	1,52	1,52
24	P49366	Deoxyhypusine synthase	DHPS	40,9	5,36	1,77	1,63
25	P11388	DNA topoisomerase 2-alpha	TOP2A	174,3	8,72	2,10	runter
26	Q96EY1	DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	52,5	9,26	2,39	3,15
27	Q99543	DnaJ homolog subfamily C member 2	DNAJC2	72,0	8,70	0,43	1,62
28	Q08477	Docosahexaenoic acid omega-hydroxylase CYP4F3	CYP4F3	59,8	7,64	3,09	0,41
29	Q02750	Dual specificity mitogen-activated protein kinase kinase 1	MAP2K1	43,4	6,62	runter	0,25
30	P36507	Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	44,4	6,55	3,46	0,52
31	Q9UJW0	Dynactin subunit 4	DCTN4	52,3	7,34	runter	0,56
32	Q96C19	EF-hand domain-containing protein D2	EFHD2	26,7	5,20	0,62	2,35
33	P06730	Eukaryotic translation initiation factor 4E	EIF4E	25,1	6,15	3,34	0,13
34	Q15056	Eukaryotic translation initiation factor 4H	EIF4H	27,4	7,23	0,47	2,24
35	P51648	Fatty aldehyde dehydrogenase	ALDH3A2	54,8	7,88	0,62	0,59
36	P52926	High mobility group protein HMGI-C	HMGA2	11,8	10,62	0,30	1,51
37	P68431	Histone H3.1	HIST1H3A	15,4	11,12	1,84	0,35
38	Q71DI3	Histone H3.2	HIST2H3A	15,4	11,27	1,95	0,25
39	Q16543	Hsp90 co-chaperone Cdc37	CDC37	44,4	5,25	0,44	1,72
40	Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HADH	34,3	8,85	1,69	1,51
41	P80217	Interferon-induced 35 kDa protein	IFI35	31,5	6,09	0,60	1,64
42	Q9H0B6	Kinesin light chain 2	KLC2	68,9	7,15	hoch	hoch
43	P09960	Leukotriene A-4 hydrolase	LTA4H	69,2	6,18	0,44	0,66
44	O94776	Metastasis-associated protein MTA2	MTA2	75,0	9,66	0,43	9,95
45	Q9NX63	MIC complex subunit MIC19	CHCHD3	26,1	8,28	0,42	3,44
46	Q66K74	Microtubule-associated protein 1S	MAP1S	112,1	7,30	0,64	0,61
47	P49821	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	50,8	8,21	runter	2,15
48	Q9BXJ9	N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	101,2	7,42	1,93	2,28
49	Q9BYT8	Neurolysin, mitochondrial	NLN	80,6	6,64	2,55	1,55
50	**P40261**	**Nicotinamide N-methyltransferase**	**NNMT**	**29,6**	**5,74**	**30,34**	**36,73**
51	Q15155	Nodal modulator 1	NOMO1	134,2	5,81	0,50	0,44
52	Q5JPE7	Nodal modulator 2	NOMO2	139,4	5,76	0,45	0,44
53	P69849	Nodal modulator 3	NOMO3	134,0	5,67	0,45	0,44

						Faktor mock vs. NNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**Caki-2 100 µM**	**Caki-2 20 µM**
54	P35658	Nuclear pore complex protein Nup214	NUP214	213,5	7,47	hoch	0,33
55	Q9NQR4	Omega-amidase NIT2	NIT2	30,6	7,21	0,61	0,30
56	Q96AY3	Peptidyl-prolyl cis-trans isomerase FKBP10	FKBP10	64,2	5,62	0,47	0,38
57	O95394	Phosphoacetylglucosamine mutase	PGM3	59,8	6,25	1,52	1,51
58	Q9HBI6	Phylloquinone omega-hydroxylase CYP4F11	CYP4F11	60,1	6,73	1,56	0,60
59	Q9UHG3	Prenylcysteine oxidase 1	PCYOX1	56,6	6,18	0,65	runter
60	Q2NL82	Pre-rRNA-processing protein TSR1 homolog	TSR1	91,8	7,42	runter	runter
61	Q8N0Y7	Probable phosphoglycerate mutase 4	PGAM4	28,8	6,65	1,65	2,30
62	P17252	Protein kinase C alpha type	PRKCA	76,7	7,05	0,46	0,38
63	Q15437	Protein transport protein Sec23B	SEC23B	86,4	6,89	2,58	4,76
64	Q9H3U1	Protein unc-45 homolog A	UNC45A	103,0	6,07	0,32	1,68
65	Q6P996	Pyridoxal-dependent decarboxylase domain-containing protein 1	PDXDC1	86,7	5,38	0,25	1,91
66	Q15293	Reticulocalbin-1	RCN1	38,9	5,00	0,63	1,53
67	Q9NQC3	Reticulon-4	RTN4	129,9	4,50	2,55	0,43
68	Q5JTH9	RRP12-like protein	RRP12	143,6	8,75	4,94	0,13
69	Q92599	Septin-8	39692	55,7	6,28	0,35	0,63
70	P84103	Serine/arginine-rich splicing factor 3	SRSF3	19,3	11,65	0,44	1,67
71	Q13177	Serine/threonine-protein kinase PAK 2	PAK2	58,0	5,96	0,57	0,64
72	P50454	Serpin H1	SERPINH1	46,4	8,69	0,66	1,98
73	O76094	Signal recognition particle subunit SRP72	SRP72	74,6	9,26	3,55	2,44
74	P63208	S-phase kinase-associated protein 1	SKP1	18,6	4,54	0,43	1,98
75	Q14683	Structural maintenance of chromosomes protein 1A	SMC1A	143,1	7,64	1,61	2,14
76	Q9NTJ3	Structural maintenance of chromosomes protein 4	SMC4	147,1	6,79	0,66	runter
77	Q969G3	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	SMARCE1	46,6	4,88	0,16	0,05
78	O00161	Synaptosomal-associated protein 23	SNAP23	23,3	5,01	1,56	3,76
79	Q12846	Syntaxin-4	STX4	34,2	6,28	hoch	hoch
80	P52888	Thimet oligopeptidase	THOP1	78,8	6,05	1,80	runter
81	P62328	Thymosin beta-4	TMSB4X	5,1	5,06	0,57	1,99
82	O14776	Transcription elongation regulator 1	TCERG1	123,8	8,65	0,27	13,16
83	P20290	Transcription factor BTF3	BTF3	22,2	9,38	0,56	1,73
84	O43493	Trans-Golgi network integral membrane protein 2	TGOLN2	51,1	5,73	0,65	0,36
85	Q9HD45	Transmembrane 9 superfamily member 3	TM9SF3	67,8	7,21	1,73	0,26
86	Q93009	Ubiquitin carboxyl-terminal hydrolase 7	USP7	128,2	5,55	0,62	0,31
87	Q14376	UDP-glucose 4-epimerase	GALE	38,3	6,73	1,69	1,65
88	Q16222	UDP-N-acetylhexosamine pyrophosphorylase	UAP1	58,7	6,33	0,45	0,37

						Faktor mock vs. NNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**Caki-2 100 µM**	**Caki-2 20 µM**
89	Q9UM54	Unconventional myosin-VI	MYO6	149,6	8,53	3,67	1,66

Tabelle S13: Gemeinsame differenziell exprimierte Proteine von transient transfizierten 786-O Zellen bei 100 µM und 20 µM Methionin (sisc *vs*. siNNMT)

						Faktor sisc *vs.* siNNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**786-O 100 µM**	**786-O 20 µM**
1	Q9Y6K5	2'-5'-oligoadenylate synthase 3	OAS3	121,1	8,40	runter	runter
2	P43686	26S protease regulatory subunit 6B	PSMC4	47,3	5,21	0,34	1,52
3	O75832	26S proteasome non-ATPase regulatory subunit 10	PSMD10	24,4	6,10	1,67	hoch
4	Q9Y676	28S ribosomal protein S18b, mitochondrial	MRPS18B	29,4	9,38	0,66	0,62
5	P82675	28S ribosomal protein S5, mitochondrial	MRPS5	48,0	9,92	0,32	runter
6	O95861	3'(2'),5'-bisphosphate nucleotidase 1	BPNT1	33,4	5,69	runter	runter
7	Q9BYD6	39S ribosomal protein L1, mitochondrial	MRPL1	36,9	8,78	runter	1,77
8	P25398	40S ribosomal protein S12	RPS12	14,5	7,21	0,47	1,57
9	P62263	40S ribosomal protein S14	RPS14	16,3	10,05	0,49	0,40
10	P62244	40S ribosomal protein S15a	RPS15A	14,8	10,13	0,46	0,66
11	P21589	5'-nucleotidase	NT5E	63,3	7,03	2,57	1,96
12	P27635	60S ribosomal protein L10	RPL10	24,6	10,08	0,54	0,58
13	P61254	60S ribosomal protein L26	RPL26	17,2	10,55	1,58	0,30
14	Q9UNX3	60S ribosomal protein L26-like 1	RPL26L1	17,2	10,55	2,78	0,35
15	P46779	60S ribosomal protein L28	RPL28	15,7	12,02	3,47	0,60
16	P62888	60S ribosomal protein L30	RPL30	12,8	9,63	0,59	0,64
17	Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic	ACAT2	41,3	6,92	1,99	1,84
18	Q53H12	Acylglycerol kinase, mitochondrial	AGK	47,1	8,09	0,57	0,48
19	O43865	Adenosylhomocysteinase 2	AHCYL1	58,9	6,89	0,41	0,56
20	P54819	Adenylate kinase 2, mitochondrial	AK2	26,5	7,81	0,53	1,65
21	P00568	Adenylate kinase isoenzyme 1	AK1	21,6	8,63	0,60	2,08
22	Q8N6H7	ADP-ribosylation factor GTPase-activating protein 2	ARFGAP2	56,7	7,99	runter	runter
23	P05091	Aldehyde dehydrogenase, mitochondrial	ALDH2	56,3	7,05	runter	0,44
24	P15121	Aldose reductase	AKR1B1	35,8	6,98	0,38	0,56
25	P30533	Alpha-2-macroglobulin receptor-associated protein	LRPAP1	41,4	8,78	0,22	2,40
26	Q06481	Amyloid-like protein 2	APLP2	86,9	4,79	runter	0,33
27	O14617	AP-3 complex subunit delta-1	AP3D1	130,1	8,48	0,47	0,54
28	P53396	ATP-citrate synthase	ACLY	120,8	7,33	1,71	1,75
29	P08237	ATP-dependent 6-phosphofructokinase, muscle type	PFKM	85,1	7,99	runter	runter

						Faktor sisc vs. siNNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**786-O 100 µM**	**786-O 20 µM**
30	Q86XP3	ATP-dependent RNA helicase DDX42	DDX42	102,9	7,02	runter	0,39
31	P35613	Basigin	BSG	42,2	5,66	0,55	0,54
32	Q562R1	Beta-actin-like protein 2	ACTBL2	42,0	5,59	5247,09	13,90
33	O95340	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2	PAPSS2	69,5	8,03	0,52	0,55
34	P80723	Brain acid soluble protein 1	BASP1	22,7	4,63	2,59	3,05
35	P27708	CAD protein	CAD	242,8	6,46	0,56	0,66
36	O75746	Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	74,7	8,38	0,56	runter
37	Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	74,1	8,62	0,53	0,52
38	P07384	Calpain-1 catalytic subunit	CAPN1	81,8	5,67	0,65	0,51
39	P00918	Carbonic anhydrase 2	CA2	29,2	7,40	0,36	0,28
40	Q9H3Q1	Cdc42 effector protein 4	CDC42EP4	38,0	5,19	runter	hoch
41	Q9Y696	Chloride intracellular channel protein 4	CLIC4	28,8	5,59	0,29	0,44
42	P83916	Chromobox protein homolog 1	CBX1	21,4	4,93	hoch	hoch
43	Q14839	Chromodomain-helicase-DNA-binding protein 4	CHD4	217,9	5,86	1,66	1,57
44	Q07021	Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	31,3	4,84	0,57	0,62
45	Q9H5V8	CUB domain-containing protein 1	CDCP1	92,9	7,96	hoch	6,24
46	Q00534	Cyclin-dependent kinase 6	CDK6	36,9	6,46	hoch	hoch
47	P49589	Cysteine--tRNA ligase, cytoplasmic	CARS	85,4	6,76	0,59	1,61
48	P14854	Cytochrome c oxidase subunit 6B1	COX6B1	10,2	7,05	0,49	1,66
49	P49366	Deoxyhypusine synthase	DHPS	40,9	5,36	hoch	5,03
50	Q96PD2	Discoidin, CUB and LCCL domain-containing protein 2	DCBLD2	85,0	7,17	0,42	0,63
51	Q92878	DNA repair protein RAD50	RAD50	153,8	6,89	4,67	runter
52	P46977	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	80,5	8,07	0,56	0,42
53	O95793	Double-stranded RNA-binding protein Staufen homolog 1	STAU1	63,1	9,44	0,60	0,39
54	Q14203	Dynactin subunit 1	DCTN1	141,6	5,81	0,62	0,54
55	Q63HN8	E3 ubiquitin-protein ligase RNF213	RNF213	591,0	6,48	0,41	0,55
56	O94874	E3 UFM1-protein ligase 1	UFL1	89,5	6,79	runter	runter
57	P42892	Endothelin-converting enzyme 1	ECE1	87,1	5,88	runter	0,52
58	P84090	Enhancer of rudimentary homolog	ERH	12,3	5,92	0,46	1,91
59	P29317	Ephrin type-A receptor 2	EPHA2	108,2	6,23	1,99	1,65
60	Q8N766	ER membrane protein complex subunit 1	EMC1	111,7	7,66	2,11	2,34
61	O94905	Erlin-2	ERLIN2	37,8	5,62	hoch	hoch
62	Q96HE7	ERO1-like protein alpha	ERO1A	54,4	5,68	1,52	2,08

						Faktor sisc vs. siNNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**786-O 100 µM**	**786-O 20 µM**
63	P30042	ES1 protein homolog, mitochondrial	C21orf33	28,2	8,27	2,51	2,97
64	P38919	Eukaryotic initiation factor 4A-III	EIF4A3	46,8	6,73	0,49	1,67
65	P63241	Eukaryotic translation initiation factor 5A-1	EIF5A	16,8	5,24	0,59	1,53
66	Q6IS14	Eukaryotic translation initiation factor 5A-1-like	EIF5AL1	16,8	5,00	0,59	2,16
67	Q9GZV4	Eukaryotic translation initiation factor 5A-2	EIF5A2	16,8	5,58	0,59	2,20
68	Q9Y5B9	FACT complex subunit SPT16	SUPT16H	119,8	5,66	0,61	0,47
69	Q96CS3	FAS-associated factor 2	FAF2	52,6	5,62	1,53	3,56
70	Q96AC1	Fermitin family homolog 2	FERMT2	77,8	6,70	0,58	0,22
71	P02751	Fibronectin	FN1	262,5	5,71	0,33	0,47
72	O75955	Flotillin-1	FLOT1	47,3	7,49	0,32	0,31
73	Q9NQ88	Fructose-2,6-bisphosphatase TIGAR	TIGAR	30,0	7,69	3,27	3,40
74	Q13630	GDP-L-fucose synthase	TSTA3	35,9	6,60	0,51	0,65
75	P78347	General transcription factor II-I	GTF2I	112,3	6,39	0,29	0,61
76	Q99988	Growth/differentiation factor 15	GDF15	34,1	9,66	hoch	hoch
77	P0DMV9	Heat shock 70 kDa protein 1B	HSPA1B	70,0	5,66	2,80	1,55
78	Q92598	Heat shock protein 105 kDa	HSPH1	96,8	5,39	1,63	1,59
79	Q9NRV9	Heme-binding protein 1	HEBP1	21,1	5,80	0,18	1,98
80	P08581	Hepatocyte growth factor receptor	MET	155,4	7,33	runter	runter
81	Q92522	Histone H1x	H1FX	22,5	10,76	hoch	2,00
82	P62805	Histone H4	HIST1H4A	11,4	11,36	0,55	0,48
83	Q86X55	Histone-arginine methyltransferase CARM1	CARM1	65,8	6,73	runter	runter
84	Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HADH	34,3	8,85	1,65	1,57
85	P26006	Integrin alpha-3	ITGA3	116,5	6,77	0,39	0,43
86	P05362	Intercellular adhesion molecule 1	ICAM1	57,8	7,99	1,95	2,23
87	P19525	Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	62,1	8,40	0,48	0,60
88	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic	IDH1	46,6	7,01	0,37	0,64
89	Q14739	Lamin-B receptor	LBR	70,7	9,36	2,49	2,00
90	Q13724	Mannosyl-oligosaccharide glucosidase	MOGS	91,9	8,90	2,10	0,61
91	Q14676	Mediator of DNA damage checkpoint protein 1	MDC1	226,5	5,47	4,60	3,29
92	Q9UNF1	Melanoma-associated antigen D2	MAGED2	64,9	9,32	0,27	0,41
93	Q96T76	MMS19 nucleotide excision repair protein homolog	MMS19	113,2	6,35	0,33	0,46
94	Q99685	Monoglyceride lipase	MGLL	33,2	6,99	0,64	0,65
95	O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	DDAH1	31,1	5,81	runter	runter
96	Q86SF2	N-acetylgalactosaminyltransferase 7	GALNT7	75,3	7,11	runter	runter

						Faktor sisc vs. siNNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**786-O 100 µM**	**786-O 20 µM**
97	P15559	NAD(P)H dehydrogenase [quinone] 1	NQO1	30,8	8,88	0,51	0,51
98	P48163	NADP-dependent malic enzyme	ME1	64,1	6,13	0,56	0,46
99	Q15758	Neutral amino acid transporter B(0)	SLC1A5	56,6	5,48	2,28	1,81
100	Q6PIU2	Neutral cholesterol ester hydrolase 1	NCEH1	45,8	7,23	1,58	1,51
101	**P40261**	**Nicotinamide N-methyltransferase**	**NNMT**	**29,6**	**5,74**	**0,09**	**runter**
102	Q9Y266	Nuclear migration protein nudC	NUDC	38,2	5,38	1,62	1,58
103	P57740	Nuclear pore complex protein Nup107	NUP107	106,3	5,43	0,18	runter
104	P52948	Nuclear pore complex protein Nup98-Nup96	NUP98	197,5	6,40	0,35	runter
105	P37198	Nuclear pore glycoprotein p62	NUP62	53,2	5,31	0,41	2,13
106	P22059	Oxysterol-binding protein 1	OSBP	89,4	7,30	runter	0,62
107	Q9BZF1	Oxysterol-binding protein-related protein 8	OSBPL8	101,1	6,96	1,83	hoch
108	Q96HC4	PDZ and LIM domain protein 5	PDLIM5	63,9	8,21	0,47	0,52
109	P30405	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	PPIF	22,0	9,38	0,49	0,17
110	Q96AY3	Peptidyl-prolyl cis-trans isomerase FKBP10	FKBP10	64,2	5,62	0,36	0,55
111	Q8IWS0	PHD finger protein 6	PHF6	41,3	8,68	0,25	0,30
112	P23634	Plasma membrane calcium-transporting ATPase 4	ATP2B4	137,8	6,60	hoch	2,49
113	P13796	Plastin-2	LCP1	70,2	5,43	1,91	1,76
114	Q15149	Plectin	PLEC	531,5	5,96	0,41	0,65
115	P09874	Poly [ADP-ribose] polymerase 1	PARP1	113,0	8,88	0,44	0,52
116	Q9H074	Polyadenylate-binding protein-interacting protein 1	PAIP1	53,5	4,81	2,04	1,51
117	O95758	Polypyrimidine tract-binding protein 3	PTBP3	59,7	9,04	runter	runter
118	Q14914	Prostaglandin reductase 1	PTGR1	35,8	8,29	2,11	1,97
119	Q5VYK3	Proteasome-associated protein ECM29 homolog	ECM29	204,2	7,12	0,47	0,34
120	Q8IVF2	Protein AHNAK2	AHNAK2	616,2	5,36	hoch	0,63
121	Q9H694	Protein bicaudal C homolog 1	BICC1	104,8	8,54	0,37	0,55
122	P49257	Protein ERGIC-53	LMAN1	57,5	6,77	0,47	0,65
123	Q86UE4	Protein LYRIC	MTDH	63,8	9,32	2,04	1,50
124	Q92734	Protein TFG	TFG	43,4	5,10	0,31	0,40
125	Q15437	Protein transport protein Sec23B	SEC23B	86,4	6,89	hoch	0,46
126	O94855	Protein transport protein Sec24D	SEC24D	112,9	7,25	0,56	0,37
127	O94979	Protein transport protein Sec31A	SEC31A	132,9	6,89	0,20	0,41
128	Q6P996	Pyridoxal-dependent decarboxylase domain-containing protein 1	PDXDC1	86,7	5,38	0,54	0,65
129	Q9NVS9	Pyridoxine-5'-phosphate oxidase	PNPO	30,0	7,06	runter	0,44
130	P52306	Rap1 GTPase-GDP dissociation stimulator 1	RAP1GDS1	66,3	5,31	1,60	2,47
131	P61019	Ras-related protein Rab-2A	RAB2A	23,5	6,54	0,48	0,51
132	Q15286	Ras-related protein Rab-35	RAB35	23,0	8,29	4,00	runter

						Faktor sisc vs. siNNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**786-O 100 µM**	**786-O 20 µM**
133	Q9NQC3	Reticulon-4	RTN4	129,9	4,50	0,51	2,04
134	P00352	Retinal dehydrogenase 1	ALDH1A1	54,8	6,73	0,31	0,58
135	Q07960	Rho GTPase-activating protein 1	ARHGAP1	50,4	6,29	0,40	0,52
136	Q8N392	Rho GTPase-activating protein 18	ARHGAP18	74,9	6,44	0,60	0,54
137	Q14137	Ribosome biogenesis protein BOP1	BOP1	83,6	6,19	2,10	0,36
138	Q9Y3A5	Ribosome maturation protein SBDS	SBDS	28,7	8,75	1,98	1,82
139	Q9BWF3	RNA-binding protein 4	RBM4	40,3	7,08	1,71	2,35
140	Q5JTH9	RRP12-like protein	RRP12	143,6	8,75	2,44	0,63
141	P34896	Serine hydroxymethyltransferase, cytosolic	SHMT1	53,0	7,71	0,66	runter
142	Q13247	Serine/arginine-rich splicing factor 6	SRSF6	39,6	11,43	4,38	0,60
143	O75914	Serine/threonine-protein kinase PAK 3	PAK3	62,3	5,45	hoch	0,52
144	Q14738	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	69,9	8,13	1,96	runter
145	Q13362	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform	PPP2R5C	61,0	6,87	1,96	runter
146	Q9BRF8	Serine/threonine-protein phosphatase CPPED1	CPD1	35,5	6,20	runter	runter
147	A0MZ66	Shootin-1	SHTN1	71,6	5,33	0,43	0,44
148	P08240	Signal recognition particle receptor subunit alpha	SRPRA	69,8	8,95	0,37	0,21
149	P42224	Signal transducer and activator of transcription 1-alpha/beta	STAT1	87,3	6,05	0,59	0,65
150	Q13596	Sorting nexin-1	SNX1	59,0	5,15	runter	runter
151	P19623	Spermidine synthase	SRM	33,8	5,49	0,58	0,49
152	Q15637	Splicing factor 1	SF1	68,3	8,98	1,56	1,89
153	Q15427	Splicing factor 3B subunit 4	SF3B4	44,4	8,56	16,06	3,37
154	Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial	SQRDL	49,9	9,11	0,49	0,58
155	O75940	Survival of motor neuron-related-splicing factor 30	SMNDC1	26,7	7,24	0,47	1,72
156	O43396	Thioredoxin-like protein 1	TXNL1	32,2	4,96	1,54	1,67
157	P07996	Thrombospondin-1	THBS1	129,3	4,94	runter	runter
158	P48307	Tissue factor pathway inhibitor 2	TFPI2	26,9	8,53	2,33	3,34
159	P20290	Transcription factor BTF3	BTF3	22,2	9,38	runter	2,01
160	Q04206	Transcription factor p65	RELA	60,2	5,68	runter	3,99
161	Q00577	Transcriptional activator protein Pur-alpha	PURA	34,9	6,44	hoch	2,02
162	P02786	Transferrin receptor protein 1	TFRC	84,8	6,61	0,63	0,63
163	Q15629	Translocating chain-associated membrane protein 1	TRAM1	43,0	9,63	0,66	0,44
164	Q9Y3B3	Transmembrane emp24 domain-containing protein 7	TMED7	25,2	6,89	0,43	runter
165	Q9Y5L0	Transportin-3	TNPO3	104,1	5,57	0,62	0,59
166	P29144	Tripeptidyl-peptidase 2	TPP2	138,3	6,32	1,56	1,54

						Faktor sisc vs. siNNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**786-O 100 µM**	**786-O 20 µM**
167	Q6IBS0	Twinfilin-2	TWF2	39,5	6,84	0,27	0,54
168	Q96DI7	U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	39,3	8,10	runter	runter
169	P45974	Ubiquitin carboxyl-terminal hydrolase 5	USP5	95,7	5,03	0,59	0,56
170	Q92890	Ubiquitin fusion degradation protein 1 homolog	UFD1L	34,5	6,70	2,22	2,13
171	P05161	Ubiquitin-like protein ISG15	ISG15	17,9	7,44	0,49	0,60
172	Q9NT62	Ubiquitin-like-conjugating enzyme ATG3	ATG3	35,8	4,74	hoch	1,54
173	P19224	UDP-glucuronosyltransferase 1-6	UGT1A6	60,7	8,41	0,42	runter
174	Q03405	Urokinase plasminogen activator surface receptor	PLAUR	37,0	6,65	hoch	hoch
175	P50552	Vasodilator-stimulated phosphoprotein	VASP	39,8	8,94	2,01	1,51
176	Q9UI12	V-type proton ATPase subunit H	ATP6V1H	55,8	6,48	1,97	1,54
177	Q969S3	Zinc finger protein 622	ZNF622	54,2	6,15	hoch	hoch

Tabelle S14: Gemeinsame differenziell exprimierte Proteine von transient transfizierten 769-P Zellen bei 100 µM und 20 µM Methionin (mock *vs*. NNMT)

						Faktor mock *vs.* NNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**769-P 100 µM**	**769-P 20 µM**
1	P51665	26S proteasome non-ATPase regulatory subunit 7	PSMD7	37,0	6,77	1,99	10,33
2	P46779	60S ribosomal protein L28	RPL28	15,7	12,02	2,48	1,56
3	Q8NE71	ATP-binding cassette sub-family F member 1	ABCF1	95,9	6,80	1,51	3,90
4	Q9NVP1	ATP-dependent RNA helicase DDX18	DDX18	75,4	9,50	1,99	0,59
5	Q7L1Q6	Basic leucine zipper and W2 domain-containing protein 1	BZW1	48,0	5,92	1,55	8,77
6	Q9NYF8	Bcl-2-associated transcription factor 1	BCLAF1	106,1	9,98	hoch	0,45
7	Q562R1	Beta-actin-like protein 2	ACTBL2	42,0	5,59	0,13	0,07
8	Q9Y6D6	Brefeldin A-inhibited guanine nucleotide-exchange protein 1	ARFGEF1	208,6	5,85	10,89	0,39
9	O75844	CAAX prenyl protease 1 homolog	ZMPSTE24	54,8	7,49	0,64	1,53
10	O43852	Calumenin	CALU	37,1	4,64	1,63	0,63
11	P13861	cAMP-dependent protein kinase type II-alpha regulatory subunit	PRKAR2A	45,5	5,07	runter	runter
12	O43809	Cleavage and polyadenylation specificity factor subunit 5	NUDT21	26,2	8,82	0,38	hoch
13	Q12996	Cleavage stimulation factor subunit 3	CSTF3	82,9	8,12	0,64	1,71
14	Q14019	Coactosin-like protein	COTL1	15,9	5,67	0,62	0,47
15	Q96A33	Coiled-coil domain-containing protein 47	CCDC47	55,8	4,87	0,17	2,80

						Faktor mock vs. NNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**769-P 100 µM**	**769-P 20 µM**
16	Q96GG9	DCN1-like protein 1	DCUN1D1	30,1	5,34	1,59	hoch
17	Q9UII4	E3 ISG15--protein ligase HERC5	HERC5	116,8	7,65	hoch	2,31
18	Q9UBQ5	Eukaryotic translation initiation factor 3 subunit K	EIF3K	25,0	4,93	0,59	1,83
19	P23588	Eukaryotic translation initiation factor 4B	EIF4B	69,1	5,73	0,48	1,56
20	P02792	Ferritin light chain	FTL	20,0	5,78	0,46	runter
21	P16930	Fumarylacetoacetase	FAH	46,3	6,95	2,65	0,63
22	P57764	Gasdermin-D	GSDMD	52,8	5,08	1,77	1,60
23	P23378	Glycine dehydrogenase (decarboxylating), mitochondrial	GLDC	112,7	7,11	0,59	8,73
24	P52926	High mobility group protein HMGI-C	HMGA2	11,8	10,62	0,60	1,70
25	O00629	Importin subunit alpha-3	KPNA4	57,9	4,96	0,66	2,51
26	O60684	Importin subunit alpha-7	KPNA6	60,0	4,98	2,02	0,62
27	P27361	Mitogen-activated protein kinase 3	MAPK3	43,1	6,74	0,57	1,59
28	**P40261**	**Nicotinamide N-methyltransferase**	**NNMT**	**29,6**	**5,74**	**5,43**	**13,65**
29	P57740	Nuclear pore complex protein Nup107	NUP107	106,3	5,43	0,54	0,66
30	Q14978	Nucleolar and coiled-body phosphoprotein 1	NOLC1	73,6	9,47	1,87	1,57
31	O75475	PC4 and SFRS1-interacting protein	PSIP1	60,1	9,13	hoch	1,53
32	P62942	Peptidyl-prolyl cis-trans isomerase FKBP1A	FKBP1A	11,9	8,16	0,54	0,53
33	Q8IWS0	PHD finger protein 6	PHF6	41,3	8,68	2,43	1,50
34	P28070	Proteasome subunit beta type-4	PSMB4	29,2	5,97	0,56	0,34
35	Q8NCA5	Protein FAM98A	FAM98A	55,4	9,03	hoch	1,76
36	Q58FG0	Putative heat shock protein HSP 90-alpha A5	HSP90AA5P	38,7	6,57	2,79	0,52
37	Q6P996	Pyridoxal-dependent decarboxylase domain-containing protein 1	PDXDC1	86,7	5,38	1,57	4,24
38	Q9NQG5	Regulation of nuclear pre-mRNA domain-containing protein 1B	RPRD1B	36,9	5,97	0,17	runter
39	Q9BRF8	Serine/threonine-protein phosphatase CPPED1	CPD1	35,5	6,20	0,43	1,57
40	P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	PPP1CB	37,2	6,19	runter	7,87
41	Q15005	Signal peptidase complex subunit 2	SPCS2	25,0	8,47	runter	0,59
42	P08240	Signal recognition particle receptor subunit alpha	SRPRA	69,8	8,95	0,19	runter
43	P05026	Sodium/potassium-transporting ATPase subunit beta-1	ATP1B1	35,0	8,53	4,53	0,36
44	Q9H2G2	STE20-like serine/threonine-protein kinase	SLK	142,6	5,15	0,61	1,51
45	P42285	Superkiller viralicidic activity 2-like 2	SKIV2L2	117,7	6,52	4,25	hoch
46	O43172	U4/U6 small nuclear ribonucleoprotein Prp4	PRPF4	58,4	7,42	0,53	2,08
47	Q93009	Ubiquitin carboxyl-terminal hydrolase 7	USP7	128,2	5,55	2,09	2,54
48	Q9HAW9	UDP-glucuronosyltransferase 1-8	UGT1A8	59,7	7,68	runter	runter

Tabelle S15: Gemeinsame differenziell exprimierte Proteine von transient transfizierten HEK-293, Caki-2 und 769-P Zellen bei 100 µM Methionin (mock *vs*. NNMT)

						Faktor mock *vs.* NNMT		
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**HEK-293 100 µM**	**Caki-2 100 µM**	**769-P 100 µM**
1	Q9Y6E2	Basic leucine zipper and W2 domain-containing protein 2	BZW2	48,1	6,68	3,46	0,58	2,40
2	Q562R1	Beta-actin-like protein 2	ACTBL2	42,0	5,59	36,00	26,52	0,13
3	Q14839	Chromodomain-helicase-DNA-binding protein 4	CHD4	217,9	5,86	0,57	1,72	1,69
4	P23588	Eukaryotic translation initiation factor 4B	EIF4B	69,1	5,73	0,45	0,64	0,48
5	Q16576	Histone-binding protein RBBP7	RBBP7	47,8	5,05	1,85	2,05	0,60
6	O00629	Importin subunit alpha-3	KPNA4	57,9	4,96	2,30	2,82	0,66
7	Q9BYT8	Neurolysin, mitochondrial	NLN	80,6	6,64	0,60	2,55	0,61
8	**P40261**	**Nicotinamide N-methyltransferase**	**NNMT**	**29,6**	**5,74**	**hoch**	**30,34**	**5,43**
9	P57740	Nuclear pore complex protein Nup107	NUP107	106,3	5,43	0,39	5,43	0,54
10	Q9NQR4	Omega-amidase NIT2	NIT2	30,6	7,21	1,71	0,61	0,60
11	Q9H3U1	Protein unc-45 homolog A	UNC45A	103,0	6,07	1,57	0,32	0,53
12	Q6P996	Pyridoxal-dependent decarboxylase domain-containing protein 1	PDXDC1	86,7	5,38	1,76	0,25	1,57
13	Q9H6Z4	Ran-binding protein 3	RANBP3	60,2	4,78	0,65	hoch	0,51
14	Q16629	Serine/arginine-rich splicing factor 7	SRSF7	27,4	11,82	0,56	runter	1,56
15	Q969G3	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	SMARCE1	46,6	4,88	5,16	0,16	7,45
16	Q9BTV4	Transmembrane protein 43	TMEM43	44,8	8,13	0,52	0,31	0,33
17	Q93009	Ubiquitin carboxyl-terminal hydrolase 7	USP7	128,2	5,55	0,25	0,62	2,09
18	Q16222	UDP-N-acetylhexosamine pyrophosphorylase	UAP1	58,7	6,33	2,06	0,45	hoch

Tabelle S16: Gemeinsame differenziell exprimierte Proteine von transient transfizierten HEK-293, Caki-2 und 769-P Zellen bei 20 µM Methionin (mock vs. NNMT)

						Faktor mock *vs.* NNMT		
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**HEK-293 100 µM**	**Caki-2 100 µM**	**769-P 100 µM**
1	O43809	Cleavage and polyadenylation specificity factor subunit 5	NUDT21	26,2	8,82	0,27	hoch	hoch
2	Q99543	DnaJ homolog subfamily C member 2	DNAJC2	72,0	8,70	runter	1,62	0,61
3	O60684	Importin subunit alpha-7	KPNA6	60,0	4,98	hoch	0,57	0,62
4	P40261	Nicotinamide N-methyltransferase	NNMT	29,6	5,74	hoch	36,73	13,65
5	Q15155	Nodal modulator 1	NOMO1	134,2	5,81	1,70	0,44	0,66
6	Q5JPE7	Nodal modulator 2	NOMO2	139,4	5,76	1,70	0,44	0,66
7	P69849	Nodal modulator 3	NOMO3	134,0	5,67	1,70	0,44	0,66
8	O75475	PC4 and SFRS1-interacting protein	PSIP1	60,1	9,13	0,50	hoch	1,53
9	Q8NCA5	Protein FAM98A	FAM98A	55,4	9,03	1,56	0,45	1,76
10	P42285	Superkiller viralicidic activity 2-like 2	SKIV2L2	117,7	6,52	0,53	0,49	hoch
11	P04350	Tubulin beta-4A chain	TUBB4A	49,6	4,88	2,33	1,72	2,22
12	O43172	U4/U6 small nuclear ribonucleoprotein Prp4	PRPF4	58,4	7,42	0,28	0,21	2,08
13	Q93009	Ubiquitin carboxyl-terminal hydrolase 7	USP7	128,2	5,55	1,56	0,31	2,54

Tabelle S17: Gemeinsame differenziell exprimierte Proteine von transient transfizierten Caki-1 und 786-O Zellen bei 100 µM Methionin (sisc *vs*. siNNMT)

						Faktor sisc *vs.* siNNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**Caki-1 100 µM**	**786-O 100 µM**
1	Q16698	2,4-dienoyl-CoA reductase, mitochondrial	DECR1	36,0	9,28	0,31	0,58
2	Q9Y676	28S ribosomal protein S18b, mitochondrial	MRPS18B	29,4	9,38	0,46	0,66
3	P51398	28S ribosomal protein S29, mitochondrial	DAP3	45,5	8,88	0,54	0,60
4	Q9NP92	28S ribosomal protein S30, mitochondrial	MRPS30	50,3	7,97	0,66	2,58
5	O95861	3'(2'),5'-bisphosphate nucleotidase 1	BPNT1	33,4	5,69	0,56	runter
6	Q9BYD6	39S ribosomal protein L1, mitochondrial	MRPL1	36,9	8,78	1,59	runter
7	P62244	40S ribosomal protein S15a	RPS15A	14,8	10,13	0,59	0,46
8	P23396	40S ribosomal protein S3	RPS3	26,7	9,66	0,42	0,44
9	Q9BRK5	45 kDa calcium-binding protein	SDF4	41,8	4,86	2,10	2,45

						Faktor sisc *vs.* siNNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**Caki-1 100 µM**	**786-O 100 µM**
10	P49189	4-trimethylaminobutyraldehyde dehydrogenase	ALDH9A1	53,8	5,87	2,73	3,19
11	P40429	60S ribosomal protein L13a	RPL13A	23,6	10,93	0,44	0,60
12	P62750	60S ribosomal protein L23a	RPL23A	17,7	10,45	2,90	2,12
13	P61254	60S ribosomal protein L26	RPL26	17,2	10,55	1,88	1,58
14	Q9UNX3	60S ribosomal protein L26-like 1	RPL26L1	17,2	10,55	2,16	2,78
15	P46779	60S ribosomal protein L28	RPL28	15,7	12,02	10,02	3,47
16	Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic	ACAT2	41,3	6,92	hoch	1,99
17	P24752	Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	45,2	8,85	0,59	0,50
18	Q9BTT0	Acidic leucine-rich nuclear phosphoprotein 32 family member E	ANP32E	30,7	3,85	0,52	0,57
19	P46108	Adapter molecule crk	CRK	33,8	5,55	0,65	0,42
20	O43865	Adenosylhomocysteinase 2	AHCYL1	58,9	6,89	1,93	0,41
21	P62330	ADP-ribosylation factor 6	ARF6	20,1	8,95	0,62	runter
22	Q8N6H7	ADP-ribosylation factor GTPase-activating protein 2	ARFGAP2	56,7	7,99	1,58	runter
23	P15121	Aldose reductase	AKR1B1	35,8	6,98	1,92	0,38
24	P30533	Alpha-2-macroglobulin receptor-associated protein	LRPAP1	41,4	8,78	1,69	0,22
25	Q06481	Amyloid-like protein 2	APLP2	86,9	4,79	2,16	runter
26	Q9BZZ5	Apoptosis inhibitor 5	API5	59,0	7,34	0,33	runter
27	P08243	Asparagine synthetase [glutamine-hydrolyzing]	ASNS	64,3	6,86	runter	0,52
28	Q12797	Aspartyl/asparaginyl beta-hydroxylase	ASPH	85,8	5,01	0,64	2,53
29	P53396	ATP-citrate synthase	ACLY	120,8	7,33	1,81	1,71
30	P08237	ATP-dependent 6-phosphofructokinase, muscle type	PFKM	85,1	7,99	2,15	runter
31	P61769	Beta-2-microglobulin	B2M	13,7	6,52	2,42	0,47
32	Q562R1	Beta-actin-like protein 2	ACTBL2	42,0	5,59	0,04	5247,09
33	O95340	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2	PAPSS2	69,5	8,03	0,35	0,52
34	P80723	Brain acid soluble protein 1	BASP1	22,7	4,63	1,75	2,59
35	P07384	Calpain-1 catalytic subunit	CAPN1	81,8	5,67	0,54	0,65
36	P17655	Calpain-2 catalytic subunit	CAPN2	79,9	4,98	0,45	0,66
37	Q9Y696	Chloride intracellular channel protein 4	CLIC4	28,8	5,59	0,59	0,29
38	P53675	Clathrin heavy chain 2	CLTCL1	186,9	5,85	0,66	0,66
39	Q14677	Clathrin interactor 1	CLINT1	68,2	6,42	1,73	0,54
40	O43809	Cleavage and polyadenylation specificity factor subunit 5	NUDT21	26,2	8,82	0,55	0,05
41	Q14019	Coactosin-like protein	COTL1	15,9	5,67	2,37	0,62
42	Q07021	Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	31,3	4,84	0,66	0,57
43	P49589	Cysteine--tRNA ligase, cytoplasmic	CARS	85,4	6,76	0,59	0,59

						Faktor sisc *vs.* siNNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**Caki-1 100 µM**	**786-O 100 µM**
44	Q9H773	dCTP pyrophosphatase 1	DCTPP1	18,7	5,03	0,59	0,57
45	Q9Y3Z3	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	72,2	7,14	3,46	runter
46	Q13443	Disintegrin and metalloproteinase domain-containing protein 9	ADAM9	90,5	7,52	hoch	0,41
47	Q12959	Disks large homolog 1	DLG1	100,4	5,76	1,54	runter
48	Q9NRW3	DNA dC->dU-editing enzyme APOBEC-3C	APOBEC3C	22,8	7,59	1,54	1,60
49	Q92878	DNA repair protein RAD50	RAD50	153,8	6,89	5,28	4,67
50	O15446	DNA-directed RNA polymerase I subunit RPA34	CD3EAP	55,0	8,51	hoch	runter
51	Q9NZN4	EH domain-containing protein 2	EHD2	61,1	6,46	0,64	0,39
52	P42126	Enoyl-CoA delta isomerase 1, mitochondrial	ECI1	32,8	8,54	0,43	0,61
53	P38919	Eukaryotic initiation factor 4A-III	EIF4A3	46,8	6,73	0,55	0,49
54	P62495	Eukaryotic peptide chain release factor subunit 1	ETF1	49,0	5,71	0,58	1,57
55	O75821	Eukaryotic translation initiation factor 3 subunit G	EIF3G	35,6	6,13	2,23	0,65
56	Q9UIA9	Exportin-7	XPO7	123,8	6,32	0,44	runter
57	Q9Y5B9	FACT complex subunit SPT16	SUPT16H	119,8	5,66	0,64	0,61
58	Q96AC1	Fermitin family homolog 2	FERMT2	77,8	6,70	runter	0,58
59	Q13642	Four and a half LIM domains protein 1	FHL1	36,2	8,97	runter	runter
60	Q9H8Y8	Golgi reassembly-stacking protein 2	GORASP2	47,1	4,82	1,65	0,47
61	Q99988	Growth/differentiation factor 15	GDF15	34,1	9,66	2,64	hoch
62	P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	GNB1	37,4	6,00	0,64	0,55
63	O43301	Heat shock 70 kDa protein 12A	HSPA12A	74,9	6,77	0,21	runter
64	P34931	Heat shock 70 kDa protein 1-like	HSPA1L	70,3	6,02	1,64	2,40
65	Q92598	Heat shock protein 105 kDa	HSPH1	96,8	5,39	1,64	1,63
66	Q9NRV9	Heme-binding protein 1	HEBP1	21,1	5,80	1,55	0,18
67	O15347	High mobility group protein B3	HMGB3	23,0	8,37	2,12	runter
68	P52926	High mobility group protein HMGI-C	HMGA2	11,8	10,62	0,48	runter
69	Q92522	Histone H1x	H1FX	22,5	10,76	hoch	hoch
70	P62805	Histone H4	HIST1H4A	11,4	11,36	0,53	0,55
71	Q86X55	Histone-arginine methyltransferase CARM1	CARM1	65,8	6,73	runter	runter
72	Q70UQ0	Inhibitor of nuclear factor kappa-B kinase-interacting protein	IKBIP	39,3	9,17	2,02	0,59
73	Q16270	Insulin-like growth factor-binding protein 7	IGFBP7	29,1	7,90	1,60	0,44
74	P26006	Integrin alpha-3	ITGA3	116,5	6,77	0,64	0,39
75	Q13418	Integrin-linked protein kinase	ILK	51,4	8,07	1,50	0,55
76	P19525	Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	62,1	8,40	1,85	0,48

						Faktor sisc *vs.* siNNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**Caki-1 100 µM**	**786-O 100 µM**
77	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic	IDH1	46,6	7,01	0,41	0,37
78	Q13907	Isopentenyl-diphosphate Delta-isomerase 1	IDI1	26,3	6,34	1,70	0,57
79	Q14739	Lamin-B receptor	LBR	70,7	9,36	runter	2,49
80	O60488	Long-chain-fatty-acid--CoA ligase 4	ACSL4	79,1	8,38	1,85	0,17
81	Q9UNF1	Melanoma-associated antigen D2	MAGED2	64,9	9,32	1,51	0,27
82	Q7Z434	Mitochondrial antiviral-signaling protein	MAVS	56,5	5,52	0,47	runter
83	O43615	Mitochondrial import inner membrane translocase subunit TIM44	TIMM44	51,3	8,32	0,62	0,59
84	Q16539	Mitogen-activated protein kinase 14	MAPK14	41,3	5,78	2,10	runter
85	Q96T76	MMS19 nucleotide excision repair protein homolog	MMS19	113,2	6,35	1,69	0,33
86	P53985	Monocarboxylate transporter 1	SLC16A1	53,9	8,66	runter	hoch
87	O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	SLC9A3R1	38,8	5,77	1,53	0,61
88	Q86SF2	N-acetylgalactosaminyltransferase 7	GALNT7	75,3	7,11	0,36	runter
89	Q9NXA8	NAD-dependent protein deacylase sirtuin-5, mitochondrial	SIRT5	33,9	8,47	0,55	runter
90	P48163	NADP-dependent malic enzyme	ME1	64,1	6,13	2,27	0,56
91	Q15758	Neutral amino acid transporter B(0)	SLC1A5	56,6	5,48	0,51	2,28
92	**P40261**	**Nicotinamide N-methyltransferase**	**NNMT**	**29,6**	**5,74**	**0,07**	**0,09**
93	P22307	Non-specific lipid-transfer protein	SCP2	59,0	6,89	hoch	runter
94	Q9Y266	Nuclear migration protein nudC	NUDC	38,2	5,38	1,85	1,62
95	Q92621	Nuclear pore complex protein Nup205	NUP205	227,8	6,19	runter	1,66
96	P52948	Nuclear pore complex protein Nup98-Nup96	NUP98	197,5	6,40	runter	0,35
97	P37198	Nuclear pore glycoprotein p62	NUP62	53,2	5,31	1,92	0,41
98	P17480	Nucleolar transcription factor 1	UBTF	89,4	5,81	runter	runter
99	P12270	Nucleoprotein TPR	TPR	267,1	5,02	0,59	0,55
100	P22392	Nucleoside diphosphate kinase B	NME2	17,3	8,41	2,35	1,81
101	Q9NX40	OCIA domain-containing protein 1	OCIAD1	27,6	7,49	hoch	0,65
102	Q9BZF1	Oxysterol-binding protein-related protein 8	OSBPL8	101,1	6,96	runter	1,83
103	P26885	Peptidyl-prolyl cis-trans isomerase FKBP2	FKBP2	15,6	9,13	0,53	runter
104	Q15149	Plectin	PLEC	531,5	5,96	0,40	0,41
105	P09874	Poly [ADP-ribose] polymerase 1	PARP1	113,0	8,88	0,58	0,44
106	Q7L014	Probable ATP-dependent RNA helicase DDX46	DDX46	117,3	9,29	0,65	runter
107	Q53EL6	Programmed cell death protein 4	PDCD4	51,7	5,21	1,74	runter
108	P35232	Prohibitin	PHB	29,8	5,76	0,41	0,57
109	Q8IVF2	Protein AHNAK2	AHNAK2	616,2	5,36	1,78	hoch
110	Q86UE4	Protein LYRIC	MTDH	63,8	9,32	0,63	2,04
111	P41236	Protein phosphatase inhibitor 2	PPP1R2	23,0	4,74	1,56	0,64

						Faktor sisc *vs.* siNNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**Caki-1 100 µM**	**786-O 100 µM**
112	Q6NXS1	Protein phosphatase inhibitor 2-like protein 3	PPP1R2P3	23,0	4,92	1,56	0,64
113	O60361	Putative nucleoside diphosphate kinase	NME2P1	15,5	8,57	2,56	1,96
114	Q9NVS9	Pyridoxine-5'-phosphate oxidase	PNPO	30,0	7,06	runter	runter
115	O00330	Pyruvate dehydrogenase protein X component, mitochondrial	PDHX	54,1	8,66	0,16	hoch
116	P61019	Ras-related protein Rab-2A	RAB2A	23,5	6,54	0,36	0,48
117	P11233	Ras-related protein Ral-A	RALA	23,6	7,11	runter	0,46
118	P18754	Regulator of chromosome condensation	RCC1	44,9	7,52	0,49	0,66
119	Q9NQC3	Reticulon-4	RTN4	129,9	4,50	0,52	0,51
120	P00352	Retinal dehydrogenase 1	ALDH1A1	54,8	6,73	0,63	0,31
121	Q9Y3A5	Ribosome maturation protein SBDS	SBDS	28,7	8,75	2,14	1,98
122	Q8WVM8	Sec1 family domain-containing protein 1	SCFD1	72,3	6,27	runter	runter
123	Q16629	Serine/arginine-rich splicing factor 7	SRSF7	27,4	11,82	6,09	runter
124	Q9P289	Serine/threonine-protein kinase 26	STK26	46,5	5,29	0,30	0,31
125	Q9BRF8	Serine/threonine-protein phosphatase CPPED1	CPD1	35,5	6,20	runter	runter
126	Q96B97	SH3 domain-containing kinase-binding protein 1	SH3KBP1	73,1	6,62	hoch	runter
127	P42224	Signal transducer and activator of transcription 1-alpha/beta	STAT1	87,3	6,05	1,69	0,59
128	P05026	Sodium/potassium-transporting ATPase subunit beta-1	ATP1B1	35,0	8,53	hoch	runter
129	Q15738	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	NSDHL	41,9	8,06	0,49	0,53
130	Q96I99	Succinate--CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	46,5	6,39	0,64	0,51
131	P24821	Tenascin	TNC	240,7	4,89	runter	2,79
132	Q9H3N1	Thioredoxin-related transmembrane protein 1	TMX1	31,8	4,98	0,51	0,41
133	P62328	Thymosin beta-4	TMSB4X	5,1	5,06	2,01	0,52
134	Q04206	Transcription factor p65	RELA	60,2	5,68	0,36	runter
135	P02786	Transferrin receptor protein 1	TFRC	84,8	6,61	0,65	0,63
136	Q13595	Transformer-2 protein homolog alpha	TRA2A	32,7	11,27	hoch	hoch
137	Q15629	Translocating chain-associated membrane protein 1	TRAM1	43,0	9,63	0,65	0,66
138	Q92544	Transmembrane 9 superfamily member 4	TM9SF4	74,5	6,54	0,66	1,73
139	Q9Y3B3	Transmembrane emp24 domain-containing protein 7	TMED7	25,2	6,89	0,50	0,43
140	Q9Y5L0	Transportin-3	TNPO3	104,1	5,57	runter	0,62
141	P22102	Trifunctional purine biosynthetic protein adenosine-3	GART	107,7	6,70	0,48	0,54
142	Q53GS9	U4/U6.U5 tri-snRNP-associated protein 2	USP39	65,3	8,91	0,66	runter
143	Q13404	Ubiquitin-conjugating enzyme E2 variant 1	UBE2V1	16,5	7,93	1,61	2,25
144	P46939	Utrophin	UTRN	394,2	5,33	hoch	0,45

						Faktor sisc *vs.* siNNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**Caki-1 100 µM**	**786-O 100 µM**
145	P50552	Vasodilator-stimulated phosphoprotein	VASP	39,8	8,94	2,74	2,01
146	Q8IWB7	WD repeat and FYVE domain-containing protein 1	WDFY1	46,3	7,33	0,60	3,25
147	Q9GZS3	WD repeat-containing protein 61	WDR61	33,6	5,47	1,78	runter

Tabelle S18: Gemeinsame differenziell exprimierte Proteine von transient transfizierten Caki-1, Caki-2, 786-O und 769-P Zellen bei 100 µM Methionin (mock *vs*. NNMT)

						Faktor sisc *vs.* siNNMT		Faktor mock *vs.* NNMT	
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**Caki-1 100 µM**	**786-O 100 µM**	**Caki-2 100 µM**	**769-P 100 µM**
1	P46779	60S ribosomal protein L28	RPL28	15,7	12,02	10,02	3,47	0,60	2,48
2	Q562R1	Beta-actin-like protein 2	ACTBL2	42,0	5,59	0,04	5247,09	26,52	0,13
3	P52926	High mobility group protein HMGI-C	HMGA2	11,8	10,62	0,48	runter	0,30	0,60
4	Q86X55	Histone-arginine methyltransferase CARM1	CARM1	65,8	6,73	runter	runter	runter	0,52
5	**P40261**	**Nicotinamide N-methyltransferase**	**NNMT**	**29,6**	**5,74**	**0,07**	**0,09**	**30,34**	**5,43**
6	Q16629	Serine/arginine-rich splicing factor 7	SRSF7	27,4	11,82	6,09	runter	runter	1,56

Tabelle S19: Gemeinsame differenziell exprimierte Proteine von transient transfizierten Caki-2, 786-O und 769-P Zellen bei 20 µM Methionin (mock *vs*. NNMT bzw. sisc *vs*. siNNMT)

						Faktor mock *vs.* NNMT		Faktor sisc *vs.* siNNMT
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**Caki-2 20 µM**	**769-P 20 µM**	**786-O 20 µM**
1	P54819	Adenylate kinase 2, mitochondrial	AK2	26,5	7,81	0,34	0,37	1,65
2	Q5T2N8	ATPase family AAA domain-containing protein 3C	ATAD3C	46,4	9,31	0,33	0,46	1,55
3	Q9NYF8	Bcl-2-associated transcription factor 1	BCLAF1	106,1	9,98	0,38	0,45	0,65
4	P33316	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial	DUT	26,5	9,36	2,01	1,65	1,86
5	**P40261**	**Nicotinamide N-methyltransferase**	**NNMT**	**29,6**	**5,74**	**36,73**	**13,65**	**runter**
6	Q15155	Nodal modulator 1	NOMO1	134,2	5,81	0,44	0,66	1,57
7	Q5JPE7	Nodal modulator 2	NOMO2	139,4	5,76	0,44	0,66	1,57

						Faktor mock *vs.* NNMT		Faktor sisc *vs.* siNNMT
	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**Caki-2 20 µM**	**769-P 20 µM**	**786-O 20 µM**
8	P69849	Nodal modulator 3	NOMO3	134,0	5,67	0,44	0,66	1,57
9	Q6P996	Pyridoxal-dependent decarboxylase domain-containing protein 1	PDXDC1	86,7	5,38	1,91	4,24	0,65
10	Q9NQC3	Reticulon-4	RTN4	129,9	4,50	0,43	0,57	2,04
11	Q9BRF8	Serine/threonine-protein phosphatase CPPED1	CPD1	35,5	6,20	0,29	1,57	runter
12	Q12846	Syntaxin-4	STX4	34,2	6,28	hoch	hoch	1,71
13	O43493	Trans-Golgi network integral membrane protein 2	TGOLN2	51,1	5,73	0,36	0,56	0,61

Tabelle S20: Differenziell exprimierte Proteine von transient transfizierten 786-O Zellen bei 20 µM Methionin (sisc *vs*. siNNMT) (Probe 1 + 2) im Massenbereich von 80 - 96 kDa

	Identifikationscode UNIPROT	**Bezeichnung**	**Proteinidentifikation**	**MW in kDa**	**pI**	**sisc**	**siNNMT**	**Faktor sisc *vs.* siNNMT**
1	Q01813	6-phosphofructokinase type C	K6PP	85,6	7,5	0,28%	0,10%	0,38
2	Q99798	Aconitate hydratase, mitochondrial	ACON	82,4	6,85	0,16%	0,14%	0,87
3	P13798	Acylamino-acid-releasing enzyme	ACPH	81,2	5,29	0,04%	0,00%	niedrig
4	Q15057	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2	ACAP2	88,0	6,38	0,02%	0,05%	1,96
5	Q92499	ATP-dependent RNA helicase DDX1	DDX1	82,4	6,8	0,13%	0,19%	1,46
6	Q05682	Caldesmon	CALD1	93,2	5,62	0,05%	0,00%	niedrig
7	P35222	Catenin beta-1	CTNB1	85,4	5,53	0,02%	0,05%	2,30
8	O43264	Centromere/kinetochore protein zw10 homolog	ZW10	88,7	5,89	0,04%	0,06%	1,46
9	O75534	Cold shock domain-containing protein E1	CSDE1	88,9	5,88	0,03%	0,14%	4,43
10	Q96JB2	Conserved oligomeric Golgi complex subunit 3	COG3	94,0	5,39	0,05%	0,05%	0,96
11	Q9H9E3	Conserved oligomeric Golgi complex subunit 4	COG4	89,0	5,09	0,06%	0,00%	niedrig
12	Q13616	Cullin-1	CUL1	89,7	8,19	0,05%	0,02%	0,44
13	Q13618	Cullin-3	CUL3	88,8	8,68	0,05%	0,04%	0,72
14	Q93034	Cullin-5	CUL5	91,0	8,08	0,05%	0,04%	0,87
15	P49589	Cysteine--tRNA ligase, cytoplasmic	SYCC	85,3	6,32	0,04%	0,00%	niedrig

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	sisc	siNNMT	Faktor sisc *vs.* siNNMT
16	P54886	Delta-1-pyrroline-5-carboxylate synthase	P5CS	87,3	6,66	0,13%	0,06%	0,44
17	P33992	DNA replication licensing factor MCM5	MCM5	82,2	8,64	0,02%	0,04%	1,95
18	P33993	DNA replication licensing factor MCM7	MCM7	81,2	6,09	0,13%	0,18%	1,35
19	Q8IXB1	DnaJ homolog subfamily C member 10	DJC10	87,3	6,69	0,07%	0,04%	0,58
20	P49959	Double-strand break repair protein MRE11A	MRE11	80,5	5,61	0,06%	0,04%	0,62
21	Q6UWE0	E3 ubiquitin-protein ligase LRSAM1	LRSM1	83,6	5,7	0,06%	0,03%	0,55
22	O94874	E3 UFM1-protein ligase 1	UFL1	89,5	6,36	0,07%	0,02%	0,31
23	P13639	Elongation factor 2	EF2	95,2	6,42	0,05%	0,11%	2,18
24	Q9H6S3	Epidermal growth factor receptor kinase substrate 8-like protein 2	ES8L2	80,6	6,39	0,05%	0,07%	1,39
25	O95479	GDH/6PGL endoplasmic bifunctional protein	G6PE	86,8	6,86	0,05%	0,02%	0,31
26	P06396	Gelsolin	GELS	83,0	5,72	0,09%	0,06%	0,66
27	P26639	Glutamine--tRNA ligase	SYQ	83,4	6,23	0,09%	0,10%	1,20
28	P47897	Glycine--tRNA ligase	SYG	87,7	6,74	0,04%	0,00%	niedrig
29	P07900	Heat shock protein HSP 90-alpha	HS90A	84,5	4,94	0,36%	0,53%	1,46
30	P08238	Heat shock protein HSP 90-beta	HS90B	83,1	4,96	2,55%	3,10%	1,22
31	Q12906	Interleukin enhancer-binding factor 3	ILF3	95,3	8,86	0,09%	0,11%	1,27
32	P14923	Junction plakoglobin	PLAK	81,7	5,75	0,03%	0,00%	niedrig
33	Q99661	Kinesin-like protein KIF2C	KIF2C	81,2	8,06	0,02%	0,05%	3,42
34	O15066	Kinesin-like protein KIF3B	KIF3B	85,1	7,3	0,04%	0,05%	1,29
35	Q9UHB6	LIM domain and actin-binding protein 1	LIMA1	85,2	6,41	0,03%	0,06%	1,81
36	Q13724	Mannosyl-oligosaccharide glucosidase	MOGS	91,9	8,97	0,06%	0,03%	0,52
37	Q16891	Mitochondrial inner membrane protein	IMMT	80,0	5,71	0,17%	0,13%	0,79
38	Q9UDY8	Mucosa-associated lymphoid tissue lymphoma translocation protein 1	MALT1	92,1	5,47	0,00%	0,04%	hoch
39	Q96TA1	Niban-like protein 1	NIBL1	84,0	5,82	0,16%	0,14%	0,88
40	Q9NR30	Nucleolar RNA helicase 2	DDX21	87,3	9,32	0,04%	0,19%	4,40
41	Q8TCS8	Polyribonucleotide nucleotidyltransferase 1, mitochondrial	PNPT1	80,9	6,26	0,06%	0,00%	niedrig
42	Q92841	Probable ATP-dependent RNA helicase DDX17	DDX17	80,3	8,53	0,04%	0,00%	niedrig

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	sisc	siNNMT	Faktor sisc *vs.* siNNMT
43	Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	81,6	6,47	0,08%	0,00%	niedrig
44	O00469	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2	PLOD2	82,0	6,16	0,07%	0,09%	1,22
45	O60568	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	PLOD3	82,4	5,64	0,09%	0,07%	0,73
46	Q32P28	Prolyl 3-hydroxylase 1	P3H1	81,2	4,99	0,05%	0,04%	0,88
47	Q15436	Protein transport protein Sec23A	SC23A	86,0	6,63	0,04%	0,00%	niedrig
48	O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	90,9	7,12	0,11%	0,13%	1,18
49	Q6P996	Pyridoxal-dependent decarboxylase domain-containing protein 1	PDXD1	86,7	5,25	0,11%	0,09%	0,83
50	P51812	Ribosomal protein S6 kinase alpha-3	KS6A3	83,7	6,41	0,05%	0,02%	0,30
51	P42224	Signal transducer and activator of transcription 1-alpha/beta	STAT1	87,2	5,74	0,24%	0,14%	0,56
52	P40763	Signal transducer and activator of transcription 3	STAT3	87,9	5,94	0,09%	0,10%	1,13
53	Q9UH99	SUN domain-containing protein 2	SUN2	80,3	6,27	0,04%	0,00%	niedrig
54	P55072	Threonine--tRNA ligase, cytoplasmic	SYTC	89,2	5,14	0,09%	0,08%	0,89
55	P02786	Transitional endoplasmic reticulum ATPase	TERA	84,9	6,18	0,05%	0,17%	3,37
56	Q13144	Translation initiation factor eIF-2B subunit epsilon	EI2BE	80,2	4,97	0,02%	0,04%	2,28
57	Q96QK1	Vacuolar protein sorting-associated protein 35	VPS35	91,7	5,32	0,06%	0,00%	niedrig
58	P13010	X-ray repair cross-complementing protein 5	XRCC5	82,6	5,55	0,28%	0,24%	0,85
59	Q6PJT7	Zinc finger CCCH domain-containing protein 14	ZC3HE	82,9	6,99	0,00%	0,03%	hoch
60	Q9BQ52	Zinc phosphodiesterase ELAC protein 2	RNZ2	90,5	7,81	0,00%	0,04%	hoch

Tabelle S21: Differenziell exprimierte Proteine von transient transfizierten 786-O Zellen bei 20 µM Methionin (sisc *vs*. siNNMT) (Probe 3 + 4) im Massenbereich von 40 - 54 kDa

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	sisc	siNNMT	Faktor sisc *vs.* siNNMT
1	P17980	26S protease regulatory subunit 6A	PRS6A	49,2	5,13	0,14%	0,09%	0,68
2	P35998	26S protease regulatory subunit 7	PRS7	48,5	5,72	0,12%	0,10%	0,90
3	P62195	26S protease regulatory subunit 8	PRS8	45,5	7,27	0,12%	0,15%	1,26

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	sisc	siNNMT	Faktor sisc *vs.* siNNMT
4	O00231	26S proteasome non-ATPase regulatory subunit 11	PSD11	47,3	6,09	0,00%	0,05%	hoch
5	P49189	4-trimethylaminobutyraldehyde dehydrogenase	AL9A1	53,8	5,69	0,04%	0,05%	1,18
6	P52209	6-phosphogluconate dehydrogenase, decarboxylating	6PGD	53,1	6,8	0,13%	0,15%	1,12
7	P60709	Actin, cytoplasmic 1	ACTB	41,7	5,29	0,11%	0,10%	0,95
8	P30520	Adenylosuccinate synthetase isozyme 2	PURA2	50,1	6,13	0,00%	0,03%	hoch
9	Q9HDC9	Adipocyte plasma membrane-associated protein	APMAP	46,3	5,82	0,05%	0,04%	0,84
10	P61163	Alpha-centractin	ACTZ	42,6	6,19	0,00%	0,04%	hoch
11	P20073	Annexin A7	ANXA7	52,7	5,52	0,06%	0,05%	0,88
12	Q9BXS5	AP-1 complex subunit mu-1	AP1M1	48,5	6,81	0,08%	0,06%	0,69
13	Q9UBB4	Ataxin-10	ATX10	53,5	5,12	0,04%	0,05%	1,27
14	Q96EP5	DAZ-associated protein 1	DAZP1	43,4	8,73	0,06%	0,05%	0,94
15	Q13561	Dynactin subunit 2	DCTN2	44,1	5,1	0,07%	0,05%	0,74
16	P68104	Elongation factor 1-alpha 1	EF1A1	50,0	9,1	0,37%	0,17%	0,46
17	P49411	Elongation factor Tu, mitochondrial	EFTU	45,0	6,31	0,10%	0,11%	1,15
18	P60842	Eukaryotic initiation factor 4A-I	IF4A1	46,0	5,32	0,23%	0,51%	2,24
19	P38919	Eukaryotic initiation factor 4A-III	IF4A3	46,9	6,3	0,05%	0,07%	1,38
20	P41091	Eukaryotic translation initiation factor 2 subunit 3	IF2G	51,0	8,66	0,04%	0,00%	niedrig
21	P60228	Eukaryotic translation initiation factor 3 subunit E	EIF3E	52,1	5,72	0,07%	0,11%	1,50
22	O75955	Flotillin-1	FLOT1	47,4	7,08	0,04%	0,06%	1,50
23	P09104	Gamma-enolase	ENOG	47,1	4,91	0,13%	0,10%	0,81
24	P48637	Glutathione synthetase	GSHB	52,3	5,67	0,09%	0,04%	0,46
25	P52597	Heterogeneous nuclear ribonucleoprotein F	HNRPF	45,7	5,37	0,18%	0,17%	0,94
26	Q16543	Hsp90 co-chaperone Cdc37	CDC37	44,5	5,17	0,12%	0,13%	1,04
27	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic	IDHC	46,5	6,53	0,05%	0,04%	0,91
28	P22234	Multifunctional protein ADE2	PUR6	46,9	7,09	0,07%	0,12%	1,64
29	P22570	NADPH:adrenodoxin oxidoreductase, mitochondrial	ADRO	50,0	7,65	0,05%	0,00%	niedrig
30	Q8TBC4	NEDD8-activating enzyme E1 catalytic subunit	UBA3	51,7	5,3	0,05%	0,03%	0,70

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	sisc	siNNMT	Faktor sisc *vs.* siNNMT
31	Q6PIU2	Neutral cholesterol ester hydrolase 1	NCEH1	45,8	6,76	0,00%	0,03%	hoch
32	Q8IVD9	NudC domain-containing protein 3	NUDC3	40,8	5,16	0,05%	0,06%	1,07
33	Q9NTK5	Obg-like ATPase 1	OLA1	44,7	7,64	0,10%	0,12%	1,22
34	Q15645	Pachytene checkpoint protein 2 homolog	PCH2	48,6	5,73	0,06%	0,07%	1,18
35	O60664	Perilipin-3	PLIN3	46,9	5,3	0,27%	0,30%	1,11
36	Q9BY77	Polymerase delta-interacting protein 3	PDIP3	46,0	10	0,05%	0,04%	0,92
37	Q9Y312	Protein AAR2 homolog	AAR2	43,3	5,66	0,00%	0,04%	hoch
38	Q15084	Protein disulfide-isomerase A6	PDIA6	46,2	4,95	0,08%	0,11%	1,31
39	Q92597	Protein NDRG1	NDRG1	42,7	5,49	0,19%	0,13%	0,66
40	Q9Y570	Protein phosphatase methylesterase 1	PPME1	42,2	5,67	0,00%	0,04%	hoch
41	P50395	Rab GDP dissociation inhibitor beta	GDIB	50,7	6,1	0,26%	0,24%	0,90
42	P18754	Regulator of chromosome condensation	RCC1	44,8	7,17	0,05%	0,03%	0,69
43	Q07960	Rho GTPase-activating protein 1	RHG01	50,4	5,85	0,07%	0,03%	0,48
44	Q9Y230	RuvB-like 2	RUVB2	51,0	5,49	0,08%	0,03%	0,43
45	Q9NVA2	Septin-11	SEP11	49,3	6,38	0,05%	0,04%	0,86
46	Q16181	Septin-7	SEP7	50,5	8,76	0,12%	0,15%	1,21
47	P50454	Serpin H1	SERPH	44,5	8,81	0,05%	0,08%	1,70
48	Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial	SQRD	50,0		0,14%	0,05%	0,33
49	Q9Y4P3	Transducin beta-like protein 2	TBL2	49,8	9,52	0,03%	0,04%	1,22
50	P55084	Trifunctional enzyme subunit beta, mitochondrial	ECHB	47,5	9,24	0,07%	0,09%	1,23
51	Q9BQE3	Tubulin alpha-1C chain	TBA1C	49,9	4,96	0,09%	0,05%	0,61
52	P07437	Tubulin beta chain	TBB5	49,7	4,78	1,90%	1,25%	0,66
53	Q13885	Tubulin beta-2A chain	TBB2A	49,9	4,78	0,05%	0,04%	0,72
54	P68371	Tubulin beta-4B chain	TBB4B	49,8	4,79	0,16%	0,08%	0,54
55	P16989	Y-box-binding protein 3	YBOX3	40,0	9,77	0,04%	0,04%	1,01

Tabelle S22: Differenziell exprimierte Proteine von transient transfizierten 786-O Zellen bei 20 µM Methionin (sisc *vs*. siNNMT) (Probe 5 + 6) im Massenbereich von 32 - 38 kDa

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	sisc	siNNMT	Faktor sisc *vs.* siNNMT
1	Q9BYD3	39S ribosomal protein L4, mitochondrial	RM04	34,9	9,73	0,05%	0,05%	0,98
2	P05388	60S acidic ribosomal protein P0	RLA0	34,3	5,70	0,21%	0,15%	0,70
3	P46777	60S ribosomal protein L5	RL5	34,2	9,73	0,08%	0,13%	1,59
4	Q02878	60S ribosomal protein L6	RL6	32,6	10,59	0,09%	0,13%	1,43
5	P14550	Alcohol dehydrogenase [NADP(+)]	AK1A1	36,4	6,35	0,07%	0,03%	0,34
6	Q99439	Calponin-2	CNN2	33,6	6,92	0,11%	0,10%	0,84
7	P27695	DNA-(apurinic or apyrimidinic site) lyase	APEX1	35,4	8,42	0,05%	0,03%	0,65
8	P25685	DnaJ homolog subfamily B member 1	DNJB1	37,9	8,75	0,04%	0,05%	1,33
9	Q13347	Eukaryotic translation initiation factor 3 subunit I	EIF3I	36,5	5,38	0,07%	0,09%	1,37
10	P04406	Glyceraldehyde-3-phosphate dehydrogenase	G3P	35,9	8,58	0,24%	0,08%	0,35
11	P31942	Heterogeneous nuclear ribonucleoprotein H3	HNRH3	36,9	6,37	0,11%	0,07%	0,66
12	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2	37,4	8,97	0,38%	0,40%	1,07
13	P00338	L-lactate dehydrogenase A chain	LDHA	36,6	8,46	0,04%	0,00%	niedrig
14	P07195	L-lactate dehydrogenase B chain	LDHB	36,5	5,72	0,10%	0,05%	0,48
15	Q8NFH5	Nucleoporin NUP53	NUP53	34,8	9,15	0,04%	0,03%	0,87
16	O00151	PDZ and LIM domain protein 1	PDLI1	35,9	6,55	0,09%	0,10%	1,08
17	Q9NQG5	Regulation of nuclear pre-mRNA domain-containing protein 1B	RPR1B	36,8	5,72	0,05%	0,06%	1,14
18	O43396	Thioredoxin-like protein 1	TXNL1	32,1	4,84	0,04%	0,07%	1,71
19	P37837	Transaldolase	TALDO	37,5	6,36	0,05%	0,07%	1,31

Tabelle S23: Differenziell exprimierte Proteine von transient transfizierten 786-O Zellen bei 20 µM Methionin (sisc *vs*. siNNMT) (Probe 7 + 8) im Massenbereich von 25 - 29 kDa

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	sisc	siNNMT	Faktor sisc *vs.* siNNMT
1	Q9NX63	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	CHCH3	26,0	8,50	0,16%	0,15%	0,94
2	P25787	Proteasome subunit alpha type-2	PSA2	25,8	7,12	0,11%	0,09%	0,86
3	O00299	Chloride intracellular channel protein 1	CLIC1	26,8	5,09	0,05%	0,00%	niedrig
4	Q9UFN0	Protein NipSnap homolog 3A	NPS3A	28,5	9,21	0,06%	0,00%	niedirg

Tabelle S24: Differenziell exprimierte Proteine von transient transfizierten 786-O Zellen bei 20 µM Methionin (sisc *vs*. siNNMT) (Probe 9 + 10) im Massenbereich von 15 - 19 kDa

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	sisc	siNNMT	Faktor sisc *vs.* siNNMT
1	O75947	ATP synthase subunit d, mitochondrial	ATP5H	18,4	5,22	0,19%	0,14%	0,76
2	P00441	Superoxide dismutase [Cu-Zn]	SODC	15,8	5,70	0,19%	0,24%	1,27
3	P15531	Nucleoside diphosphate kinase A	NDKA	17,1	5,81	0,28%	0,38%	1,36
4	P55957	BH3-interacting domain death agonist	BID	15,2	9,29	0,21%	0,20%	0,97
5	P62750	60S ribosomal protein L23a	RL23A	17,6	10,44	0,39%	0,67%	1,72

Tabelle S25: Differenziell exprimierte Proteine von transient transfizierten Caki-1 Zellen bei 100 µM Methionin (sisc *vs*. siNNMT) (Probe 11 + 12) im Massenbereich von 68 - 88 kDa

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	sisc	siNNMT	Faktor sisc *vs.* siNNMT
1	Q01813	6-phosphofructokinase type C	K6PP	85,6	7,50	0,32%	0,18%	0,56
2	P08237	6-phosphofructokinase, muscle type	K6PF	85,1	8,23	0,05%	0,04%	0,70
3	P11021	78 kDa glucose-regulated protein	GRP78	70,5	5,01	1,45%	1,75%	1,21
4	P13798	Acylamino-acid-releasing enzyme	ACPH	81,2	5,29	0,03%	0,00%	niedrig
5	Q9NUQ8	ATP-binding cassette sub-family F member 3	ABCF3	79,6	5,96	0,09%	0,07%	0,86
6	O00571	ATP-dependent RNA helicase DDX3X	DDX3X	73,1	6,73	0,19%	0,16%	0,84
7	Q8IYB8	ATP-dependent RNA helicase SUPV3L1, mitochondrial	SUV3	85,6	7,37	0,06%	0,05%	0,73

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	sisc	siNNMT	Faktor sisc *vs.* siNNMT
8	P07384	Calpain-1 catalytic subunit	CAN1	81,8	5,49	0,24%	0,16%	0,68
9	Q12996	Cleavage stimulation factor subunit 3	CSTF3	82,8	8,26	0,11%	0,08%	0,74
10	Q13409	Cytoplasmic dynein 1 intermediate chain 2	DC1I2	71,3	5,08	0,07%	0,09%	1,29
11	P54886	Delta-1-pyrroline-5-carboxylate synthase	P5CS	87,3	6,66	0,12%	0,05%	0,42
12	Q9NY33	Dipeptidyl peptidase 3	DPP3	82,5	5,02	0,11%	0,13%	1,14
13	O00429	Dynamin-1-like protein	DNM1L	81,9	6,37	0,10%	0,09%	0,95
14	Q92945	Far upstream element-binding protein 2	FUBP2	73,0	6,84	0,21%	0,15%	0,71
15	Q96AC1	Fermitin family homolog 2	FERM2	77,9	6,26	0,08%	0,04%	0,53
16	P51114	Fragile X mental retardation syndrome-related protein 1	FXR1	69,6	5,84	0,08%	0,10%	1,21
17	Q06210	Glutamine-fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	78,7	6,68	0,10%	0,05%	0,52
18	P41250	Glycine--tRNA ligase	SYG	83,2	6,61	0,14%	0,12%	0,86
19	P49915	GMP synthase [glutamine-hydrolyzing]	GUAA	76,6	6,43	0,09%	0,08%	0,87
20	P11142	Heat shock cognate 71 kDa protein	HSP7C	70,8	5,37	0,07%	0,08%	1,25
21	Q12931	Heat shock protein 75 kDa, mitochondrial	TRAP1	73,5	6,13	0,08%	0,12%	1,59
22	P08238	Heat shock protein HSP 90-beta	HS90B	83,1	4,96	0,06%	0,10%	1,80
23	O60506	Heterogeneous nuclear ribonucleoprotein Q	HNRPQ	69,5	8,68	0,14%	0,12%	0,89
24	O43390	Heterogeneous nuclear ribonucleoprotein R	HNRPR	70,8	8,25	0,00%	0,05%	hoch
25	P14923	Junction plakoglobin	PLAK	81,7	5,75	0,06%	0,00%	niedrig
26	Q9H0B6	Kinesin light chain 2	KLC2	68,9	6,72	0,04%	0,06%	1,55
27	P42166	Lamina-associated polypeptide 2, isoform alpha	LAP2A	75,4	7,80	0,12%	0,06%	0,56
28	O60488	Long-chain-fatty-acid--CoA ligase 4	ACSL4	79,2	8,66	0,07%	0,09%	1,34
29	Q8IXI1	Mitochondrial Rho GTPase 2	MIRO2	68,1	5,55	0,04%	0,00%	niedrig
30	P28331	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUS1	77,0	5,42	0,11%	0,10%	0,97
31	Q9BZE4	Nucleolar GTP-binding protein 1	NOG1	73,8	9,52	0,05%	0,07%	1,66
32	Q9BSC4	Nucleolar protein 10	NOL10	80,3	8,64	0,00%	0,04%	hoch
33	Q96EY7	Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	74,4	5,62	0,07%	0,06%	0,94
34	P51659	Peroxisomal multifunctional enzyme type 2	DHB4	79,7	8,96	0,17%	0,13%	0,79

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	sisc	siNNMT	Faktor sisc *vs*. siNNMT
35	Q9Y263	Phospholipase A-2-activating protein	PLAP	87,2	5,96	0,07%	0,08%	1,16
36	P11940	Polyadenylate-binding protein 1	PABP1	70,7	9,52	0,29%	0,28%	0,97
37	Q13310	Polyadenylate-binding protein 4	PABP4	70,8	9,31	0,04%	0,05%	1,23
38	Q8TCS8	Polyribonucleotide nucleotidyltransferase 1, mitochondrial	PNPT1	80,9	6,26	0,04%	0,00%	niedrig
39	P02545	Prelamin-A/C	LMNA	73,8	6,57	0,25%	0,34%	1,34
40	Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	81,6	6,47	0,13%	0,12%	0,92
41	P13667	Protein disulfide-isomerase A4	PDIA4	70,7	4,89	0,47%	0,53%	1,14
42	Q15436	Protein transport protein Sec23A	SC23A	86,0	6,63	0,14%	0,10%	0,76
43	P35241	Radixin	RADI	68,6	6,03	0,13%	0,12%	0,96
44	Q9UHD2	Serine/threonine-protein kinase TBK1	TBK1	83,6	6,32	0,05%	0,03%	0,73
45	O76094	Signal recognition particle subunit SRP72	SRP72	74,5	9,31	0,06%	0,08%	1,28
46	P42224	Signal transducer and activator of transcription 1-alpha/beta	STAT1	87,2	5,74	0,09%	0,05%	0,60
47	Q15637	Splicing factor 1	SF01	68,2	9,08	0,07%	0,05%	0,71
48	P38646	Stress-70 protein, mitochondrial	GRP75	68,8	5,44	0,06%	0,11%	1,91
49	P26639	Threonine--tRNA ligase, cytoplasmic	SYTC	83,4	6,23	0,11%	0,08%	0,70
50	Q9BW92	Threonine--tRNA ligase, mitochondrial	SYTM	81,0		0,07%	0,04%	0,59
51	P40939	Trifunctional enzyme subunit alpha, mitochondrial	ECHA	79,0	8,98	0,24%	0,21%	0,89
52	Q9NQW7	Xaa-Pro aminopeptidase 1	XPP1	69,8	5,42	0,08%	0,07%	0,88

Tabelle S26: Differenziell exprimierte Proteine von transient transfizierten Caki-1 Zellen bei 100 µM Methionin (sisc *vs*. siNNMT) (Probe 13 + 14) im Massenbereich von 28 - 32 kDa

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	sisc	siNNMT	Faktor sisc *vs*. siNNMT
1	Q9NVS9	Pyridoxine-5'-phosphate oxidase	PNPO	30,0	6,61	0,12%	0,12%	1,02
2	P60174	Triosephosphate isomerase	TPIS	30,8	5,65	1,81%	1,57%	0,87

Tabelle S27: Differenziell exprimierte Proteine von transient transfizierten 769-P Zellen bei 20 µM Methionin (mock *vs*. NNMT) (Probe 15 + 16) im Massenbereich von 28 - 32 kDa

	Identifikationscode UNIPROT	Bezeichnung	Proteinidentifikation	MW in kDa	pI	mock	NNMT	Faktor mock *vs.* NNMT
1	P62258	14-3-3 protein epsilon	1433E	29,2	4,63	0,44%	0,31%	0,70
2	P61981	14-3-3 protein gamma	1433G	28,3	4,80	0,10%	0,18%	1,88
3	P61247	40S ribosomal protein S3a	RS3A	29,8	9,75	0,30%	0,16%	0,55
4	P62753	40S ribosomal protein S6	RS6	28,7	10,85	0,15%	0,09%	0,62
5	P62424	60S ribosomal protein L7a	RL7A	30,0	10,61	0,28%	0,11%	0,38
6	P47756	F-actin-capping protein subunit beta	CAPZB	31,2	5,36	0,05%	0,08%	1,50
7	O94903	Proline synthase co-transcribed bacterial homolog protein	PROSC	30,3	7,09	0,04%	0,00%	0,00
8	Q06323	Proteasome activator complex subunit 1	PSME1	28,7	5,78	0,10%	0,10%	1,03
9	Q9Y3A5	Ribosome maturation protein SBDS	SBDS	28,6	8,91	0,05%	0,07%	1,29
10	P21796	Voltage-dependent anion-selective channel protein 1	VDAC1	30,6	8,63	0,75%	0,45%	0,59